

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 25, 2005, 22:08:33 ; Search time 5981 Seconds
(without alignments)

11341.001 Million cell updates/sec

Title: US-10-070-255-4

Perfect score: 1782

Sequence: 1 atgagcgatcacagacaa.....taaatgtcttcattccttg 1782

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 69479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

- 1: gb_est1.*
- 2: gb_est2.*
- 3: gb_hic.*
- 4: gb_est3.*
- 5: gb_est4.*
- 6: gb_est5.*
- 7: gb_est6.*
- 8: gb_gss1.*
- 9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	821	46.1	1981	3	BC024293 Homo sapi
2	653.8	36.7	998	5	BQ064251 AGENCOURT
3	651.6	36.6	990	5	BQ060776 AGENCOURT
4	650	36.5	691	4	BQ668241 UI-E-CK1
5	648.2	36.4	970	5	BQ065026 AGENCOURT
6	639.8	35.9	730	1	AU122438
7	634.2	35.6	829	4	BG757448
8	627.8	35.2	835	4	BG758677
9	627.8	35.2	1022	5	BQ057616 AGENCOURT
10	624.6	35.1	843	4	BG758425
11	624.4	35.0	892	5	BQ057008
12	598	33.6	609	4	BM692924
13	574.8	32.3	813	4	BG684262
14	535	30.0	819	4	BG759681
15	534.6	30.0	626	5	BQ184171
16	521.6	29.3	620	5	BQ185857
17	513	28.8	769	4	BG684980
18	505.6	28.1	914	4	BG340557
19	500.6	27.8	951	4	BG685372
20	494.6	27.8	1064	5	BQ065934
21	491.8	27.6	1064	5	BQ065934
22	480.4	27.5	744	9	AY399018
23	478.8	26.9	737	4	BF975008
24	478.2	26.8	1075	5	BQ058038 AGENCOURT

25	471	26.4	1051	5	BQ061744
c	462.6	26.0	855	5	BX760749
26	461.2	25.9	576	2	AM974284
27	455.4	25.6	822	4	BM478075
28	453.2	25.4	965	4	BG757633
29	450.4	25.3	504	4	BM697878
c	439	24.6	439	1	AI136989
30	428.6	24.1	501	1	AL135642
31	423.8	23.8	682	9	AY399019
32	423.8	23.8	682	9	AY399019
33	406.4	22.8	419	1	AA593354
34	395	22.2	744	9	AY399020
35	384.8	21.6	430	2	AW403206
36	382.4	21.5	850	5	BQ642454
37	382.4	21.5	850	5	BQ642454
38	382	21.4	506	5	BX283539
39	373.4	21.0	522	2	AW044949
40	370.8	20.8	520	2	AW503340
41	355	19.9	478	5	BX283759
42	354.6	19.9	847	7	CR579211
43	342.4	19.2	646	1	AL965834
44	329.6	18.5	498	4	BG759800
45	326.4	18.3	658	2	BB623950

ALIGNMENTS

RESULT 1
BC024293
LOCUS BC024293 1981 bp mRNA linear HTC 04-MAR-2003
DEFINITION Homo sapiens, clone IMAGE:5088007, mRNA.
ACCESSION BC024293
VERSION BC024293.1 GI:22028130
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1981)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (26-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Nees, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smalilus, Michael Smith, Lorraine Spence, Jeff Scott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 42 Row: m Column: 22
This clone has the following problem: retained intron.

FEATURES
source
Location/Qualifiers
1. .1981
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5088007"
/tissue_type="Lymph, lymphoma"


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Db 509 AAAAAAGACACCTGGGGGAGGGGAGAGCTCAGAGGACAACTCCGACCACTCTCTGTCAAT 568
Qy 907 ATCATGTCCGCTTTTGAAGCCCTTCGGGCTTAATCCAAATGGAAGTCAAGAGCAGCAAC 966
Db 569 ATCATGTCCGCTTTTGAAGCCCTTCGGGCTTAATCCAAATGGAAGTCAAGAGCAGCAAC 628
Qy 967 TCATGGAATAATGATCCCTGTCTTTGAACGGGAGTTTGGGTACCAAGACTTGATGTG 1026
Db 629 TCGTGGAAAAATGATTCCTCTGCTTTGAACAGGAGTTTGGGTACCAAGACTTGATGTG 688
Qy 1027 AAAAGCATCGATGATGAAGATGTGGATCAAAACGAAAGTACGCTGATGGAATCTCATCA 1086
Db 689 AAAAGCATCGATGATGAAGATGTGGATGANNACGAGATGACGTGATGGAATCTCATCA 748
Qy 1087 GGAAGGAGCACAGGGGCCACTCGAGTTCGCCCGAGAA 1124
Db 749 GGACCGAAGCACAGGGGCCACTCAGAGTTCGCCCGAGAA 786
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RESULT 3

BQ060776
LOCUS BQ060776 7049038 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5816452
DEFINITION 5', mRNA sequence.

ACCESSION BQ060776.1 GI:19884191

VERSION EST.

KEYWORDS Homo sapiens (human)

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Straubeberg, Ph.D.
Email: cgaaps-remail.nih.gov
Tissue Procurement: Lou Staudt

cDNA Library Preparation: Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Cloning Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LICM2073 row: f column: 05

High quality sequence stop: 686.

Location/Qualifiers

1. 990

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5816452"

/tissue_type="lymphoma, cell line"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_99"

/notes="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:

ECORI; cDNA made by oligo-dT priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:

GGACGAG(G). Size-selected >500bp for average insert size

1.8kb. Library constructed by Ling Hong in the laboratory

of Gerald M. Rubin (University of California, Berkeley).

using ZAP-cDNA synthesis kit (Stratagene) and Superscript

II RT (Life Technologies). Note: this is a NIH_MGC

Library."

FEATURES

source

RESULT 4

BM668241/c

LOCUS

DEFINITION

UI-E-CKI-afk-h-18-0-UI.s2 UI-E-CKI Homo sapiens cDNA clone

UI-E-CKI-afk-h-18-0-UI 3', mRNA sequence.

ACCESSION BM668241

VERSION BM668241

KEYWORDS EST.

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 691)

AUTHORS

Bonaldo, M.F., Lennon, G. and Soares, M.B.

TITLE

Normalization and subtraction: two approaches to facilitate gene

discovery

JOURNAL

Genome Res. 6 (9), 791-806 (1996)

MEDLINE

97044477

PUBMED

8889548

COMMENT

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

Query Match

Best Local Similarity

36.6%; Score 651.6; DB 5; Length 990;

96.8%; Pred. No. 2.3e-164;

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@iowa.edu

Tissue Procurement: Dr. Gregg Hageman

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research

Genetics (www.resgen.com).

Seq primer: M13 Forward

POLYA=Yes.

FEATURES
source
1. .631
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-CK1-afk-h-18-0-UI"
/tissue_type="Retina foveal and Macular"
/dev_stage="adult"
/lab_host="DHI0B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-CK1"
/notes="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-E-CK1 is a normalized cDNA library containing the following tissue(s): Retina foveal and Macular. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dfr)18 tail. The sequence tag for this library is GACC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).
TAG TISSUE=Foveal and Macular Retina
TAG LIB=UI-E-CK1
TAG_SEQ=GTCC"

ORIGIN

Query Match 36.5%; Score 650; DB 4; Length 691;
Best Local Similarity 99.7%; Pred. No. 5.6e-164;
Matches 672; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
QY 1110 GGAGTCGCCGGAAGCCACTGGAAGGGAACACCTGCTCTCCAGATGCACAGCTGGGC 1169
DB 691 GGAGTCGCCGGAAGCCACTGGAAGGGAACACCTGCTCTCCAGATGCACAGCTGGGC 632
QY 1170 TCCGCTGAAGGTGCTGCACAAATGATCCCGACATCTCTTCCCTGTAGTGGGTGGGCTC 1229
DB 631 TCCGCTGAAGGTGCTGCACAAATGATCCCGACATCTCTTCCCTGTAGTGGGTGGGCTC 572
QY 1230 CTACAGCCAGCAGATGCCCCCTCGAAGCCTGGAGACGGACAGGACAGGACCA 1289
DB 571 CTACAGCCAGCAGATGCCCCCTCGAAGCCTGGAGACGGACAGGACAGGACCA 512
QY 1290 CGTTCTCCGGATCCTGGACTTCGGTACAGTGTGGAAGCCAGCTCTCCAGGCCACGGAAG 1349
DB 511 CGTTCTCCGGATCCTGGACTTCGGTACAGTGTGGAAGCCAGCTCTCCAGGCCACGGAAG 452
QY 1350 TCCTCTGAGCAGCTGTTACTTCTTGCTCAGTGCAGCAGATCCATGACATAGTAGTGAAT 1409
DB 451 TCCTCTGAGCAGCTGTTACTTCTTGCTCAGTGCAGCAGATCCATGACATAGTAGTGAAT 392
QY 1410 GCCCAGGCCACGTGGCCATGATGAACAGGAGGATGAGCTGGAGGAGGAGACAGATC 1469
DB 391 GCCCAGGCCACGTGGCCATGATGAACAGGAGGATGAGCTGGAGGAGGAGACAGATC 332
QY 1470 ACTGCGAAACCTGCTGCACGGTGAGATGGAGCACTCAGCGCGCTCCGGAAGAGGTGGA 1529
DB 1470 ACTGCGAAACCTGCTGCACGGTGAGATGGAGCACTCAGCGCGCTCCGGAAGAGGTGGA 1529

DB 331 ACTGCGAAACCTGCTGCACGGTGAGATGGAGCACTCAGCGCGCTCCGGAAGAGGTGGA 272
QY 1530 CACCTTGAAGAAAGAGTGGCTGAAACAGAGAGCGGCGAGGCATGAAGTCCAGCGCT 1589
DB 271 CACCTTGAAGAAAGAGTGGCTGAAACAGAGAGCGGCGAGGCATGAAGTCCAGCGCT 212
QY 1590 GCCCAGCTATCTTCTGCTATTTTGTGAGGAGATCTTAACCCACGTCGAGAACCATGTGGTG 1649
DB 211 GCCCAGCTATCTTCTGCTATTTTGTGAGGAGATCTTAACCCACGTCGAGAACCATGTGGTG 152
QY 1650 GAGAAATGGAGGAGAGAGAAATCCAAAGTTTCTCTGATAGTCTCATTTGAGGCTCCTGGAT 1709
DB 151 GAGAAATGGAGGAGAGAGAAAT-CAACAGTTTCTCTGATAGTCTCATTTGAGGCTCCTGGAT 93
QY 1710 CCAGTCTTCTGAGAGCTGTGTTTCTCTGAGACTTTTCTATGTATGTAG-CCAAATAAAT 1768
DB 92 CCAGTCTTCTGAGAGCTGTGTTTCTCTGAGACTTTTCTATGTATGTATGTAGGCCCAATAAT 33
QY 1769 GCTTTCATTCCTTG 1782
DB 32 GCTTTCATTCCTTG 19
BQ065026
LOCUS
DEFINITION
AGENCOURT_6856627 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5929505
5', mRNA sequence.
BQ065026
ACCESSION
VERSION
BQ065026.1 GI:19894072
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 970)
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS
NIH-MGC http://mgi.nci.nih.gov/
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-romail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM2107 row: 1 column: 18
High quality sequence stop: 676.
FEATURES
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1. .970
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/db_xref="taxon:9606"
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/tissue_type="lymphoma, cell line"
/lab_host="DHI0B (phage-resistant)"
/clone_lib="NIH MGC 99"
/notes="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 36.4%; Score 648.2; DB 5; Length 970;
Best Local Similarity 97.0%; Pred. No. 1.9e-163;
Matches 672; Conservative 0; Mismatches 18; Indels 3; Gaps 1;

427 AGCACTTTTATGAAGACTGGTCTTTTGTGATGATGAAGAAAGGTCAGTATCTCTCT 486
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Db 92 AGTACTTTTATGAAGACTGGTCTTTTGTGATGATGAAGAGAGGTCAGTATCTCTCT 151
|||
Qy 487 ACCATGGCAGCAGGTCTGAACCTCATCTCTTTGCGGATTAACATCGACAACAGGATTTG 546
Db 152 ACCATGGCAGCAGGTCTGAACCTCATCTCTTTGCGGATTAACATCGACAACAGGATTTG 211
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Qy 547 AACGGGAGAGTAAGTTTGTCTCCACCGTTTTCAGACCTCTTAAAGGAGTCAACAGCAAC 606
Db 212 AACGGGAGAGTAAGTTTGTCTCCACCGTTTTCAGACCTCTTAAAGGAGTCAACAGCAAT 271
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Qy 607 GTGACCTCTTGTCTGAAGGATCCACGCAAGGAGTGAAGCAGCTTTTTCAGGGAGATCACA 666
Db 272 GTGA---CCTTGTCTGAAGGATCCACGCAAGGAGTGAAGCAGCTTTTTCAGGGAGATCACA 328
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Qy 667 GCCTCTCTGCGCTCTCATCTCTTCACTCACTTCACTTCACTTCACTTCACTTCACTTCACT 726
Db 329 GCCTCTCTGCGCTCTCATCTCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 388
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Qy 727 GTGTCCAGGAATGTCAAGGATCCACGCAAGGAGTGAAGCAGCTTTTTCAGGGAGATCACA 786
Db 389 GTGTCCAGGAATGTCAAGGATCCACGCAAGGAGTGAAGCAGCTTTTTCAGGGAGATCACA 448
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Qy 787 GTGACCAACATAATCTCTTGTGATGATGAGGAAGATGAGCAGAACTCTTGGGGAGCTGTTT 846
Db 449 GTGACCAACATAATCTCTTGTGATGATGAGGAAGATGAGCAGAACTCTTGGGGAGCTGTTT 508
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Qy 847 AAAAAACACTGGGGAGAGGAGTCAAGAGCAAACTCCGACCGCTCTCTTGTCAAT 906
Db 509 AAAAAACACTGGGGAGAGGAGTCAAGAGCAAACTCCGACCGCTCTCTTGTCAAT 568
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Qy 907 ATCATGTCCGCTTTTGAAGCCCTTCGGGCTTAACCTCAATGAAGTCAAGAGCAAC 966
Db 569 ATCATGTCCGCTTTTGAAGCCCTTCGGGCTTAACCTCAATGAAGTCAAGAGCAAC 628
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Qy 967 TCATGGAATAATGATCCCTGTCTTTGAAGCGGGAGTTTGGGTACCAAGACTTGTATGTG 1026
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Qy 1027 AAAAAACACTGATGATGAAGATGATGATGAAGCAAACTCAATGAAGTCAAGAGCAAC 1086
Db 689 AAAAAACACTGATGATGAAGATGATGATGAAGCAAACTCAATGAAGTCAAGAGCAAC 748
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Qy 1087 GGAAGGAAGCAGCAGGGCCACTCGAGTTCGCC 1119
Db 749 GGACGGAAAGCAGCAGGGCCACTCAAGTTCGCC 781

RESULT 6
AUI22438
LOCUS
DEFINITION AUI22438 MAMMAL Homo sapiens cdna clone MAMMAL002380 5', mRNA
sequence.
ACCESSION AUI22438
VERSION AUI22438.1 GI:10937708
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 730)
AUTHORS Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,
Yanamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
Isogai, T.
TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975

Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project: 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="MAMMAL002380"
/tissue_type="mammary gland"
/clone_lib="MAMMAL"
/note="Vector: pME18SFL3"

ORIGIN

Query Match 35.9%; Score 639.8; DB 1; Length 730;
Best Local Similarity 99.0%; Pred. No. 3.3e-161;
Matches 663; Conservative 0; Mismatches 5; Indels 2; Gaps 2;
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Qy 61 GTGAAAACAGTCCAGATCCGCTTTTGGAGGGAGAAAGAGATTTGCTCGGATTTCCGACAGC 120
Db 123 GTGAAAACAGTCCAGATCCGCTTTTGGAGGGAGAAAGAGATTTGCTCGGATTTCCGACAGC 182
|||
Qy 121 AGGTTCACCTGTCTGTGTGCCCATTTTGAAGCCGTCTCTGAGCATGCTTTGAAGAGAGT 180
Db 183 AGGTTCACCTGTCTGTGTGCCCATTTTGAAGCCGTCTCTGAGCATGCTTTGAAGAGAGT 242
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Qy 181 CGAGGATTTGCACTCAAGCGGGAGCGATCAAGCAGGCGGGCTTTGGCAGCAAAACC 240
Db 243 CGAGGATTTGCACTCAAGCGGGAGCGATCAAGCAGGCGGGCTTTGGCAGCAAAACC 302
|||
Qy 241 GAAACAGAGCCGCTGTTTCTGTACTACGTGAAGAGAGTCTCTCAACAGACAGAGCTGCAG 300
Db 303 GAAACAGAGCCGCTGTTTCTGTACTACGTGAAGAGAGTCTCTCAACAGACAGAGCTGCAG 362
|||
Qy 301 CGCTTTACTCCCTGCGCCACATCGCCTCAGAGCTGGGCGGGGTCCGGCTTGGCTGGC 360
Db 363 CGCTTTACTCCCTGCGCCACATCGCCTCAGAGCTGGGCGGGGTCCGGCTTGGCTGGC 422
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Qy 361 TGTGCCCTCAACGAACACTCCCTGGAGCGTACTCGACATGCTCTGGCGGACCGCTGC 420
Db 423 TGTGCCCTCAACGAACACTCCCTGGAGCGTACTCGACATGCTCTGGCGGACCGCTGC 482
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Qy 421 AGCTCAGCACTTTTATGAAGACTGGTCTTTTGTGATGATGAAGAGTCCAGTATG 480
Db 483 AGCTCAGCACTTTTATGAAGACTGGTCTTTTGTGATGATGAAGAGTCCAGTATG 542
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Qy 481 CTCTCTACCATGGCAGAGGTCTGAATCCATCTCTTTGCGGATTAACATCGACAACAG 540
Db 543 CTCTCTACCATGGCAGAGGTCTGAATCCATCTCTTTGCGGATTAACATCGACAACAG 602
|||
Qy 541 GATTGAAACGGGAGAGTAAAGTTTGTCCACCGTTTTCAGACCTCTTAAAGGAGTCAACG 600
Db 603 GATTGAAACGGGAGAGTAAAGTTTGTCCACCGTTTTCAGACCTCTTAAAGGAGTCAACG 662
|||
Qy 601 CAGAACCTGTACCTCTTCTGCTGAAGAGTCCACGCAAGAGTGAAGCAGCTGTTTTCAGGGAG 660
Db 663 CAGAACCTGTGCTGCTGAAGAGTCCACGCAAGAGTGAAGCAGCTGTTTTCAGGGAG 720
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Qy 661 ATCACAGCCT 670
Db 721 ATCACAGCCT 730

RESULT 7
BG757448
LOCUS

BG757448 829 bp mRNA linear EST 15-MAY-2001

```

DEFINITION 602711292F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4851502 5',
            mRNA sequence.
ACCESSION  BG757448
VERSION     BG757448.1 GI:14068101
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 829)
            NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS     National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE       Unpublished (1999)
JOURNAL     Contact: Robert Strausberg, Ph.D.
COMMENT     Email: cgapbs-remail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            CDNA Library Preparation: Ling Hong/Rubin Laboratory
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1694 row: 9 column: 23
            High quality sequence stop: 801.
FEATURES    Location/Qualifiers
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            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:4851502"
            /tissue_type="primary B-cells from tonsils (cell line)"
            /lab_host="DH10B (phage-resistant)"
            /clone_lib="NIH_MGC_48"
            /note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
            Site 2: EcoRI; CDNA made by oligo-dT priming.
            Directionally cloned into EcoRI/XhoI sites using the
            following 5' adaptor: GGCACGAG(G). Size-selected >500bp
            for average insert size 1.8kb. Library constructed by Ling
            Hong in the laboratory of Gerald M. Rubin (University of
            California, Berkeley) using ZAP-cDNA synthesis kit
            (Stratagene) and Superscript II RT (Life Technologies).
            Note: this is a NIH_MGC Library."
ORIGIN
Query Match 35.6%; Score 634.2; DB 4; Length 829;
Best Local Similarity 96.1%; Pred. No. 1.1e-159;
Matches 672; Conservative 0; Mismatches 23; Indels 4; Gaps 2;

QY 427 AGCATTCTTTATGAAGACTGGTCTTTTGTGATGGATGAAGAAAGGTCCAGTATGCTTCCT 486
DB |||||||
DB 133 AGTACTTTTATGAAGACTGGTCTTTTGTGATGGATGAAGAAAGGTCCAGTATGCTTCCT 192
QY 487 ACCATGGCAGCAGGTCTGAATCCATCTCTTTGCGATTAACTCGACAAAGGATTTG 546
DB |||||||
DB 193 ACCATGGCAGCAGGTCCGAACCTCATACTCTTTGCGATTAACTCGACAAAGGATTTG 252
QY 547 AACGGGAGAGTAAGTTTGTCTCCACCGTTTTCAGACTCTTAAAGAGTCAACGAGAAC 606
DB |||||||
DB 253 AACGGGAGAGTAAGTTTGTCTCCACCGTTTTCAGACTCTTAAAGAGTCAACGAGAAC 312
QY 607 GTGACCTCTCTTGTGAAGAGTCCACGCAAGGAGTGGAGCGCTGTTTCAGGGAGATCACA 666
DB |||||||
DB 313 GTGA----CCTTGTGAAGAGTTCACCAAGGAGTGGAGCGCTGTTTCAGGGAGATCACA 369
QY 667 GCCTCTCTTCGCTCTCCATCTCTCATCAAACTTGAACAGGAGACCGACCCCTTTCGCTGTC 726
DB |||||||
DB 370 GCCTCTCTTCGCTCTCCATCTCTCATCAAACTTGAACAGGAGACCGACCCCTTTCGCTGTC 429
QY 727 GTGTCAGGAGATGTCACTGCTGATGCCAAATGCAAAAGAGCGGAGAGAGAAAGAAA 786
DB |||||||
DB 430 GTGTCCAGGAATGTCACTGCTGATGCCAAATGCAAAAGAGCGGAGAGAGAAAGAAA 489
QY 787 GTGACCAACATAATCTCATTTGATGATGAGGAAGATGAGCAGAACTCTGGGGAGCTGTTT 846

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DB 490 GTGACCAACATTTATCTCATTTGATGATGAGGAAGATGAGCAGAACTCTGGGACATGTTT 549
QY 847 AAAAAAGACACCTGGGGCAGGGAGAGCTCAGAGGACAACTCCGACCGTCTCTTGTCAAT 906
DB |||||||
DB 550 AAAAAAGACACCTGGGGCAGGGAGAGCTCAGAGGACAACTCCGACCTCTCTTGTCAAT 609
QY 907 ATCATGTCCGCTTTTGAAGAGCCCTTCGGCCCTAACTCCAATGGAAGTCAGAGCAGAAC 966
DB |||||||
DB 610 ATCATGTCCGCTTTTGAAGAGCCCTTCGGCCCTAACTCCAATGGAAGTCAGAGCAGAAC 609
QY 967 TCATGAAAAATTTGATTCCTCTCTTTTGAACCGGGAGTTTGGGTACCAGAAAGCTTGTATGTG 1026
DB |||||||
DB 670 TCGTGGAAAAATTTGATTCCTCTCTTTTGAACAGGGAGTTTGGGTACCAGAAAGCTTGTATGTG 729
QY 1027 AAAAGCATCGATGATGAAGATGTGGATGAAAACGAGATGACGTGTATGG-AAACTCATC 1085
DB |||||||
DB 730 AAAAGCATCGATGATGAAGATGTGGATGAAAACGAGATGACGTGTATGGAAGAACTCATC 789
QY 1086 AGGAAGGAGCAGACGGGCGCACTCGGAGTCGCCCGAGAA 1124
DB |||||||
DB 790 AGGACGGAAGCACATGTGTCACACTCAGAGTCGGGCGAGAA 828

RESULT 8
BG758677 835 bp mRNA linear EST 15-MAY-2001
LOCUS 602712923F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4853188 5',
DEFINITION mRNA sequence.
ACCESSION  BG758677
VERSION     BG758677.1 GI:14069330
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 835)
            NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS     National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE       Unpublished (1999)
JOURNAL     Contact: Robert Strausberg, Ph.D.
COMMENT     Email: cgapbs-remail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            CDNA Library Preparation: Ling Hong/Rubin Laboratory
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1698 row: n column: 05
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            /tissue_type="primary B-cells from tonsils (cell line)"
            /lab_host="DH10B (phage-resistant)"
            /clone_lib="NIH_MGC_48"
            /note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
            Site 2: EcoRI; CDNA made by oligo-dT priming.
            Directionally cloned into EcoRI/XhoI sites using the
            following 5' adaptor: GGCACGAG(G). Size-selected >500bp
            for average insert size 1.8kb. Library constructed by Ling
            Hong in the laboratory of Gerald M. Rubin (University of
            California, Berkeley) using ZAP-cDNA synthesis kit
            (Stratagene) and Superscript II RT (Life Technologies).
            Note: this is a NIH_MGC Library."
ORIGIN
Query Match 35.2%; Score 627.8; DB 4; Length 835;
Best Local Similarity 96.6%; Pred. No. 5.9e-158;

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Matches	675;	Conservative	0;	Mismatches	17;	Indels	7;	Gaps	3;
Qy	427	AGCACTTTTATGAAGACTGGTCTTTTGTGATGATGAAGAAAGGTCCAGTATGCTTCCT							486
Db	31	AGTACTTTTATGAAGACTGGTCTTTTGTGATGATGAAGAGGTCCAGTATGCTTCCT							90
Qy	487	ACCATGCGACAGGTCTGAACCTCATCTCTTTGCGATTAACTGCAACAAGGATTG							546
Db	91	ACCATGCGACAGGTCCGAACTCCATCTCTTTGCGATT--ATTGACAAAGGATTG							147
Qy	547	AACGGGCGAGAGTAAAGTTTGTCTCCACCGTTTCAGACCTCTTAAAGGAGTCAAGCGCAAC							606
Db	148	AACGGGCGAGAGTAAAGTTTGTCTCCACCGTTTCAGACCTCTTAAAGGAGTCAAGCGCAAT							207
Qy	607	GTGACCTCTTGTGTAAGGAGTCCACCAAGGAGTGAAGAGTCTTTCAGGGAGATCACA							666
Db	208	GTGA---CCTTGTCTGAAGGAGTCCACCAAGGAGTGAAGAGTCTTTCAGGGAGATCACA							264
Qy	667	GCCTCTCTGCGGTCTCATCTCTCAAACTGAAAGAGACCGA.CCCCTTGCCTGTC							726
Db	265	GCCTCTCTGCGGTCTCATCTCTCAAACTGAAAGAGACCGA.CCCCTTGCCTGTC							324
Qy	727	GTGTCCAGGAATGTCAGTCTGATGCCAAATGCAAAAGGAGCGGAAGAAAGAA							786
Db	325	GTGTCCAGGAATGTCAGTCTGATGCCAAATGCAAAAGGAGCGGAAGAAAGAA							384
Qy	787	GTGACCAACATAATCTCATTTGATGATGAGGAAGATGAGCAGAACTCTGGGGAGCTGTT							846
Db	385	GTGACCAACATAATCTCATTTGATGATGAGGAAGATGAGCAGAACTCTGGGGAGCTGTT							444
Qy	847	AAAAAGACACTGGGGGAGGGAGAGCTCAGAGACAACTCCGACCCGCTCTCTGTCAAT							906
Db	445	AAAAAGACACTGGGGGAGGGAGAGCTCAGAGACAACTCCGACCCGCTCTCTGTCAAT							504
Qy	907	ATCATGTCCGCTTTGAAAGCCCTTCGGGCTAACTCCAAATGGAAGTTCAGAGCAGCAAC							966
Db	505	ATCATGTCCGCTTTGAAAGCCCTTCGGGCTAACTCCAAATGGAAGTTCAGAGCAGCAAC							564
Qy	967	TCATGGAATAATGATTCCTCTGTTTGAACGGGAGTTTGGGTACCAAGAGCTTGATGTG							1026
Db	565	TCGTGGAATAATGATTCCTCTGTTTGAACAGGAGTTTGGGTACCAAGAGCTTGATGTG							624
Qy	1027	-AAAGCATGATGATGAAGATGGATGAAACGAAGATGACGTGTATGAAACTCATC							1085
Db	625	AAAGCATGATGATGAAGATGGATGAAACGAAGATGACGTGTATGAAACTCATC							684
Qy	1086	AGGAGGACACAGGGGGCACTCGGAGTCGCCCGAGAA	1124						
Db	685	AGGAGGAGACAGGGGGCACTCAGAGTCGCCCGAGAA	723						

RESULT 9
B0057616
LOCUS
DEFINITION B0057616 1022 bp mRNA linear EST 29-MAR-2002
5', mRNA sequence.
AGENCOURT 7047416 NIH_MGC_99 Homo sapiens cdna clone IMAGE:5813279
B0057616
ACCESSION B0057616.1 GI:19816956
VERSION
KEYWORDS EST.
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1022)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Lou Staudt
cdna Library Preparation: Rubin Laboratory
cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LCM2065 row: a column: 24
High quality sequence stop: 641.
Location/Qualifiers
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/clone_lib="NIH MGC 99"
/notes="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
Query Match 35.2%; Score 627.8; DB 5; Length 1022;
Best Local Similarity 96.3%; Pred. No. 6.3e-158;
Matches 654; Conservative 0; Mismatches 22; Indels 3; Gaps 1;

ORIGIN

Qy 427 AGCACTTTTATGAAGACTGGTCTTTTGTGATGATGAAGAAAGGTCCAGTATGCTTCCT 486
Db 70 AGTACTTTTATGAAGACTGGTCTTTTGTGATGATGAAGAGAGTTCAGTATGCTTCCT 129
Qy 487 ACCATGCGACAGTCTGAACCTCATCTCTTTCGATTAACTCGCAACAAGGATTG 546
Db 130 ACCATGCGACAGTCTCGAACTCATCTCTTTCGATTAACTCGCAACAAGGATTG 189
Qy 547 AACGGGCGAGTAAAGTTTGTCTCCACCGTTTCAGACCTCTTAAAGGAGTCAACGCAAG 606
Db 190 AACGGGCGAGTAAAGTTTGTCTCCACCGTTTCAGACCTCTTAAAGGAGTCAACGCAAG 249
Qy 607 GTGACCTCTTCTGAAGAGTCCACGCAAGGAGTGAAGAGCTTTCAGGGAGATCACA 666
Db 250 GTGA---CCTTGTCTGAAGGAGTCCACGCAAGGAGTGAAGAGCTTTCAGGGAGATCACA 306
Qy 667 GCCTCTCTCCGCTCTCCATCTCATCAAACTGAAACAGGAGACCGACCCCTTGCCTGTC 726
Db 307 GCCTCTCTCCGCTCTCCATCTCATCAAACTGAAACAGGAGACCGACCCCTTGCCTGTC 366
Qy 727 GTGTCCAGGAATGTCAGTCTGATGCCAAATGCAAAAGGAGCGGAAGAAAGAA 786
Db 367 GTGTCCAGGAATGTCAGTCTGATGCCAAATGCAAAAGGAGCGGAAGAAAGCA 426
Qy 787 GTGACCAACATAATCTCATTTGATGATGAGGAAGATGAGCAGAACTCTGGGGAGCTGTT 846
Db 427 GTGACCAACATAATCTCATTTGATGATGAGGAAGATGAGCAGAACTCTGGGGAGCTGTT 486
Qy 847 AAAAAGACACTGGGGGAGGGAGAGCTCAGAGACAACTCCGACCCGCTCTCTGTCAAT 906
Db 487 AAAAAGACACTGGGGGAGGGAGAGCTCAGAGACAACTCCGACCCGCTCTCTGTCAAT 546
Qy 907 ATCATGTCCGCTTTGAAAGCCCTTCGGGCTAACTCCAAATGGAAGTCAAGAGCAGCAAC 966
Db 547 ATCATGTCCGCTTTGAAAGCCCTTCGGGCTAACTCCAAATGGAAGTCAAGAGCAGCAAC 606
Qy 967 TCATGGAATAATGATTCCTCTGTTTGAACGGGAGTTTGGGTACCAAGAGCTTGATGTG 1026
Db 607 TCGTGGAAATGATTCCTCTGTTTGAACAGGAGTTTGGGGACCAAGAGCTTGATGTG 666
Qy 1027 AAAAGCATGATGATGAAGATGGATGAAACGAAGATGACGTGTATGGAACCTCATCA 1086
Db 667 AAAAGCATGATGATGAAGATGGATGAAACGAAGATGACGTGTATGGAACCTCATCA 726

of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

ORIGIN	Query Match 35.0%; Score 624.4; DB 5; Length 892; Best Local Similarity 92.4%; Pred. No. 5e-157; Matches 680; Conservative 0; Mismatches 51; Indels 5; Gaps 2;	
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Db	98 AGTACTTTTATGAAGACTGGTCTTTTGTGATGATGAAGAAAGTCCAGTATGCTTCT 157	
Qy	487 ACCATGGCAGAGGTCTGAATCCCATCTTTTGGATTAAATCATGCAACAAGGATTG 546	
Db	158 ACCATGGCAGAGGTCCCACTCCATCTTTTGGATTAAATCATGCAACAAGGATTG 217	
Qy	547 AACGGGACAGTAAAGTTTGTCTCCACCTTTTCAGACCTTTAAAGGAGTCAACGAGAAC 606	
Db	218 AACGGGACAGTAAAGTTTGTCTCCACCTTTTCAGACCTTTAAAGGAGTCAACGAGAAC 277	
Qy	607 GTGACCTCTTGTGAAGAGTCCACGCAAGAGTGACAGCTGTTTCAGGAGATCACA 666	
Db	278 GTGA---CCTTGTGAGAGTCCACGCAAGAGTGACAGCTGTTTCAGGAGATCACA 334	
Qy	667 GCCTCTCTGCGCTCTCCATCTCATCAAACTGAAACAGAGAGACGACCCCTTGCCTGTC 726	
Db	335 GCCTCTCTGCGCTCTCCATCTCATCAAACTGAAACAGAGAGACGACCCCTTGCCTGTC 394	
Qy	727 GTGTCCAGGAATGTCAGTCTGATGCCAAATGCAAAAGAGCGGAGAAAGAAAGAAA 786	
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Qy	787 GTGACCAACAATCTCTATTTGATGATCAGGAAGATGACAGAACTCTGGGAGCTGTTT 846	
Db	455 GTGACCAACAATCTCTATTTGATGATGAGGAAGATGACAGAACTCTGGGAGCATGTTT 514	
Qy	847 AAAAAGACACCTGGGGAGGGAGAGCTCAGAGGACAACTCCGACCGCTCTCTGTCTCAAT 906	
Db	515 AAAAAGACACCTGGGGAGGGAGAGCTCAGAGGACAACTCCGACCGCTCTCTGTCTCAAT 574	
Qy	907 ATCATGTCGGCTTTGAAAGCCCTTCCGGCTTAATCTCAATGGAAGTCAAGAGCAAC 966	
Db	575 ATCATGTCGGCTTTGAAAGCCCTTCCGGCTTAATCTCAATGGAAGTCAAGAGCAAC 634	
Qy	967 TCATGGAAAATGATTCCTCTGCTTTGAAACGGGAGTTTGGGTACCAGAACTTGTATGTG 1026	
Db	635 TCGTGGAAAATGATTCCTCTGCTTTGAAACGGGAGTTTGGGTACCAGAACTTGTATGTG 694	
Qy	1027 AAAAGCATCGATGATGAAGATGTGGATGAAAACGAAGATGACGTGTATGGAACCTCATCA 1086	
Db	695 AAAAGCATCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 754	
Qy	1087 GGAA--GGAAGCAGAGGGCCACTCGGAGTCCCGGAGAACCACTGGAAGGGAAACACT 1144	
Db	755 GGGACGGAAGGCCAGGGGCCACTCCGAGATCCCGCGCAGAAAAACGGAACACACTTCT 814	
Qy	1145 GCCTCTCCAGATGCA 1160	
Db	815 GTCACCCCGCTGGA 830	
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LOCUS	BM692924	609 bp mRNA linear EST 28-FEB-2002
DEFINITION	UI-E-CK1-afk-h-18-0-UI.r1 UI-E-CK1 Homo sapiens cDNA clone	
ACCESSION	BM692924	
VERSION	BM692924.1	GI:19006182
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	

REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	1 (bases 1 to 609)	
TITLE	Bonaldo,M.F., Lennon,G. and Soares,M.B.	
JOURNAL	Normalization and subtraction: two approaches to facilitate gene discovery	
MEDLINE	Genome Res. 6 (9), 791-806 (1996)	
PUBMED	97044477	
COMMENT	8889548	
CONTACT	Contact: Soares, MB	
COORDINATED	Coordinated Laboratory for Computational Genomics	
UNIVERSITY	University of Iowa	
ADDRESS	375 Newton Road, 4156 MEBRP, Iowa City, IA 52242, USA	
TEL	Tel: 319 335 8250	
FAX	Fax: 319 335 9565	
EMAIL	Email: bento-soares@uiowa.edu	
CDNA	Tissue Procurement: Dr. Gregg Hageman	
CDNA	CDNA Library preparation: Dr. M. Bento Soares, University of Iowa	
CDNA	CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa	
CDNA	CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa	
CDNA	Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).	
SEQ	Seq primer: M13 Reverse.	
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ORIGIN		
Query Match	33.6%; Score 598; DB 4; Length 609;	
Best Local Similarity	99.8%; Pred. No. 6.1e-150;	
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Qy	1160 ACAGCTGGCTCCGCTGAAGTCTGCACATGATCGACATCTCTTCCCTGTCACTG 1219	
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Qy	1280 CAGAGGACCACTGTTCTCCCGGATCCTGGATCTCGGTACAGTGTGGAAGCCAGCTCTCCAG 1339	
Db	181 CAGAGGACCACTGTTCTCCCGGATCCTGGATCTCGGTACAGTGTGGAAGCCAGCTCTCCAG 240	
Qy	1340 GCCACGGAAGTCTCTCAGCAGACCTGTTACCTTCTGCTCTAGTCCAGAGTCCATGACAA 1399	

Db 241 GCCACGGAAGTCTCTGAGCAGCCTGTTACCTTCTGCCTCAGTGCCAGAGTCCATGACAA 300
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 Db 421 AAGAGGTGGACACCTTTGAAAGGAAGGTGGCTGAAACAGGAGGAGCGCAGGCGCATGAAG 480
 Qy 1580 TCAGGCGCTGGCAGCCTATCTTTTGTCTATTTTGTGAGGAGATTCTAACCCCGCTGAGAA 1639
 Db 481 TCAGGCGCTGGCAGCCTATCTTTTGTCTATTTTGTGAGGAGATTCTAACCCCGCTGAGAA 540
 Qy 1640 CCATGTGGTGGAGAAATGGAGGAGAGAGAAATCCACAGATTCCTCATAGTCTCATTTGA 1699
 Db 541 CCATGTGGTGGAGAAATGGAGGAGAGAGAAAT-CAACAGTTCCTGATAGTCTCATTTGA 599
 Qy 1700 GCTCTCTGGAT 1709
 Db 600 GCTCTCTGGAT 609

RESULT 13

BG684262

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

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 602635896F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4763783 5',
 mRNA sequence.
 BG684262.1 GI:13915659
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 813)
 NIH-MGC http://mgs.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCMI619 row: p column: 24
 High quality sequence stop: 795.

FEATURES

source

1..813
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 /tissue="types"primary B-cells from consils (cell line)"
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 /clone_lib="NIH_MGC_48"
 /notes="Organ: B-cells; Vector: pOTB7; Site:1: XhoI;
 Site:2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCAGGAG(G). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

ORIGIN

Query Match 32.3%; Score 574.8; DB 4; Length 813;
 Best Local Similarity 96.3%; Pred. No. 1.2e-143;
 Matches 653; Conservative 0; Mismatches 17; Indels 8; Gaps 6;
 Qy 427 AGCACATTTTATGACAGACTGGTCTTTTGTGATGGATGAAGAAGGTCCAGATGCTTCCT 486
 Db 142 AGTACTTTTATGACAGACTGGTCTTTTGTGATGGATGAAGAAGGTCCAGATGCTTCCT 200
 Qy 487 ACCATGGCAGCAGGTCTGAACCTCCATCTCTTTTGGGATTAAACATCGACAACAGGATTTG 546
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 Qy 547 AACGGGCAGAGTAAGTTTGTCTCCACCGTTTTCAGACCTCTTAAAGAGTCAACGAGAAC 606
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 Qy 607 GTGACCTCTTGTGAAGGAGTCCACGCAAGGAGTGCAGCAGCTGTTCAGGGAGATCACA 666
 Db 321 GTGA----CTTGTCTGAAGGAGTCCACGCAAGGAGTGCAGCAGCTGTTCAGGGAGATCACA 377
 Qy 667 GCTCTCTTCCCGTCTCCATCTCTCATCAAAACCTGAAACAGAGACCAACCTCTTCCCTGTC 726
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 Qy 727 GTGTCAGGAATGTCACTGCTGATGCCAAATGCCAAAAGAGCGGAAGAAAAGAA 786
 Db 438 GTGTCAGGAATGTCACTGCTGATGCCAAATGCCAAAAGAGCGGAAGAAAAGCAA 497
 Qy 787 GTGACCAACATATCTCATTTTGTATGATGAGGAAGATGACGAGAACTCTGGGACGTTT 846
 Db 498 GTGACCAACATATCTCATTTTGTATGATGAGGAAGATGACGAGAACTCTGGGACGTTT 557
 Qy 847 AAAAAA-CACCTGGGCGAGGGAGAGCTCAGAGGACAACTCCGACCGCTCTCTCTGCAA 905
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 Qy 906 TATCATGTCGGCTTTTGAAGCCCTTCCGGCTTAATCTCAATGGAAGTCAGAGGACAA 965
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 Db 677 CTCGTGAAAAATTTGGATTCCCTGCTTTTGAACAGGGAG-TTGGGTACCAAGACCTTGATG 735
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 RESULT 14
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 602713374F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4853346 5',
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 BG759681.1 GI:14070334
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 819)
 NIH-MGC http://mgs.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Place: LNCMI699 row: d column: 19
High quality sequence stop: 791.
Location/Qualifiers

1. 819
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4853346"
/tissue="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 48"
/note="Organ: B-cells; Vector: pOTB7; Site1: XhoI;
Site2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 30.0%; Score 535; DB 4; Length 819;
Best Local Similarity 95.4%; Pred. No. 7e-133;
Matches 617; Conservative 0; Mismatches 20; Indels 10; Gaps 6;
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Qy 177 AGTACTTTTATGAAGACTGGTCTTTTGTGATGATGAAGAAGTCCAGTATGCTTCT 236
Db |||
Qy 487 ACCATGGCAGAGGTCTGAATCCATATCTTTTGGATTAAATCGACAAACAAGATTG 546
Db |||
Qy 237 ACCATGGCAGAGGTCCGAATCCATATCTTTTGGATTAAATCGACAAACAAGATTG 296
Qy 547 AACGGCAGAGTAACTTTGCTCCACCGTTTCAGACCTTTAAAGGAGTCAACGAGAC 606
Db |||
Qy 297 AACGGCAGAGTAACTTTGCTCCACCGTTTCAGACCTTTAAAGGAGTCAACGAGAA 356
Qy 607 GTGACCTCTTCTGTAAGAGTCCACGCAAGAGTGAAGAGTGGAGGAGATCACA 666
Db |||
Qy 357 GTGA---CTTGTGAAGAGTCCACGCAAGAGTGAAGAGTGGAGGAGATCACA 413
Qy 667 GCCTCTCTGCGCTCTCATCTCATCAAACTGAAAGAGGAGAGCCCTTGTGCTGTC 726
Db |||
Qy 414 GCCTCTCTGCGCTCTCATCTCATCAAACTGAAAGAGGAGAGCCCTTGTGCTGTC 473
Qy 727 GTGTCCAGAGTGCAGTCTGATGCCAAATGCAAAAGAGGAGCGGAAGAAAGAA 786
Db |||
Qy 474 GTGTCCAGAGTGCAGTCTGATGCCAAATGCAAAAGAGGAGCGGAAGAAAGAA 533
Qy 787 GTGACCAACATAATCTCATTTGATGATGAGGAAGTGAAGAGTCTGGGGAGCTGTT 846
Db |||
Qy 534 GTGACCAACATAATCTCATTTGATGATGAGGAAGTGAAGAGTCTGGGGAGCTGTT 593
Qy 847 -AAAAAGACACTGGGGAGGGAGAGCTCAGAGGACAACTCCAGCCCTCTCTGTCAA 905
Db |||
Qy 594 AAAAAAGACACTGGGGAGGGAGAGCTCAGAGGACAACTCCAGCCCTCTCTGTCAA 653
Qy 906 TATCATGTCGCCCTTTGAAGCCCTTCGGGCCCTTAATCCATGGAAGTCAAGAGCA 965
Db |||
Qy 654 TATCATGTCGCCCTTTGAAG--CCCTTCGGGCCCTTAATCCATGGAAGTCAAGAGCA 712
Qy 966 CTC-ATGGAATAATGATTCCTCTGTC--TTTGAACGGGGAGTTGGGTACCAAGAGCTTGA 1022
Db |||
Qy 713 CTCGTGGAATAATGATTCCTCTGTC--TTTGAACGGGGAGTTGGGTACCAAGAGCTTGA 772
Qy 1023 TGTGAAAGCATCGATGATGAAGATGT--GGATGAAACGAAGATGA 1067

Db 773 TGTGAAAGCATCGATGATGAAGATGTGGGATGAAACGAAGATTA 819
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RESULT 15
BQ184171/c
LOCUS
DEFINITION
UI-E-EJ1-ajs-e-23-0-UI.81 UI-E-EJ1 Homo sapiens cDNA clone
UI-E-EJ1-ajs-e-23-0-UI 3', mRNA sequence.
626 bp mRNA linear EST 30-APR-2002

ACCESSION
BQ184171
VERSION
BQ184171.1 GI:20359722
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 626)
REFERENCE
AUTHORS
TITLE
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
889548
JOURNAL
MEDLINE
PUBMED
COMMENT

Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

source
1..626
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="UI-E-EJ1-ajs-e-23-0-UI"
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optic nerve, retina, Retina Foveal and Macular, RPE and
Choroid"
/dev_stage="fetal and adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-EJ1"
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-E-EJ1 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT73-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes,
AGATTCAAGA; lens, CGATTAGCGA; eye anterior segment,
AATGCCGAT; optic nerve, CCATTAGTG; retina, CCGCG; Retina
Foveal and Macular, CTCG; RPE and Choroid, ACCTA. This
library was created for the program, Gene Discovery in the
Visual System, supported by National Eye Institute (NEI).
TAG_TISSUE=human retina
TAG_LIB=UI-E-EJ1
TAG_SEQ=CCGCG"

ORIGIN

Query Match 30.0%; Score 534.6; DB 5; Length 626;

Best Local Similarity 99.1%; Pred. No. 8.3e-133;		Matches 537; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	
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QY	305	TCTACTCCCTGCGCCACATCGCTCAGAGTGGCGGGTCCGCTGGCTGGCTGGCTGG	364
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Db	424	CCCTCAACGAACACTCCCTGGAGCGTACCTGCACATGCTCTGGCGGACCGCTGCAGGC	365
QY	425	TGAGCACTTTTATGAAGACTGCTCTTTGTGTGATGATGAAGAAAGTCCAGTATGCTTC	484
Db	364	TGAGCACTTTTATGAAGACTGCTCTTTGTGTGATGATGAAGAAAGTCCAGTATGCTTC	305
QY	485	CTACCATGGCAGCAGGTCTGAACCTCACTCTTTGCGATTACATCGACAAAGGATT	544
Db	304	CTACCATGGCAGCAGGTCTGAACCTCACTCTTTGCGATTACATCGACAAAGGATT	245
QY	545	TGAACGGCGCAGAGTAAGTTTGTCTCCACCGCTTTTCAGACCTCTTAAAGGAGTCAACGAGA	604
Db	244	TGAACGGCGCAGAGTAAGTTTGTCTCCACCGCTTTTCAGACCTCTTAAAGGAGTCAACGAGA	185
QY	605	ACGTGACCTCTTGTGTAAGAGTCCACGCAAGAGTGAAGCAGCCTGTTTCAGGGAGATCA	664
Db	184	ACGTGACCTCTTGTGTAAGAGTCCACGCAAGAGTGAAGCAGCCTGTTTCAGGGAGATCA	125
QY	665	CAGCCTCCTCTGCGGTCTCCATCCTCATCAACCTGACAGGAGACCGACCCCTTGCCCTG	724
Db	124	CAGCCTCCTCTGCGGTCTCCATCCTCATCAACCTGACAGGAGACCGACCCCTTGCCCTG	65
QY	725	TCGTGTCCAGGAATGTCAGTGTGATGCCAAATGCAAAAGGAGCGGAAGAAAAAGA	784
Db	64	TCGTGTCCAGGAATGTCAGTGTGATGCCAAATGCAAAAGGAGCGGAAGAAAAAGA	5
QY	785	AA 786	
Db	4	AA 3	

Search completed: October 26, 2005, 05:49:54
Job time : 5988 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 25, 2005, 21:11:53 ; Search time 1482 Seconds
(without alignments)
9923.208 Million cell updates/sec

Title: US-10-070-255-4
Perfect score: 1782
Sequence: 1 atgagcgatcacagacaa.....taaatgtcttcattccttg 1782

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9772377 seqs, 4126317084 residues

Total number of hits satisfying chosen parameters: 19544754

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
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- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
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- 18: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
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- 21: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq.*
- 22: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq.*
- 23: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
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- 25: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 26: /cgn2_6/ptodata/2/pubpna/US11_PUBCOMB.seq.*
- 27: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 28: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	275.8	15.5	280	9	US-09-563-817-201
2	247	13.9	454	24	US-10-450-763-214
C 3	227.8	12.8	542	17	US-10-029-386-8542
C 4	224.8	12.6	284	17	US-10-029-386-22242
5	207.6	11.6	463	24	US-10-450-763-28004

6	206.8	11.6	465	26	US-11-060-756-3234	Sequence 3234, Ap
7	206.8	11.6	465	26	US-11-060-756-7506	Sequence 7506, Ap
C 8	143.8	8.1	492	13	US-09-925-065A-383678	Sequence 383678, Ap
C 9	135.4	7.6	474	24	US-10-450-763-9353	Sequence 9353, Ap
10	128	7.2	500	17	US-10-029-386-8336	Sequence 8336, Ap
11	124	7.0	124	17	US-10-029-386-22036	Sequence 22036, A
C 12	119	6.7	911	24	US-10-450-763-215	Sequence 215, App
13	75	4.2	633	13	US-09-925-065A-681221	Sequence 681221, A
14	66.8	3.7	1796	26	US-11-097-143-11288	Sequence 11288, A
C 15	66.8	3.7	3796	26	US-11-097-143-11287	Sequence 11287, A
C 16	63.8	3.6	3931	19	US-10-276-774-948	Sequence 948, App
17	63	3.5	16536	24	US-10-981-277-35	Sequence 35, Appl
18	54.4	3.1	813	24	US-10-450-763-21166	Sequence 21166, A
C 19	54.4	3.1	79977	24	US-10-737-082-58	Sequence 58, Appl
C 20	54.4	3.1	79977	24	US-10-765-790-58	Sequence 58, Appl
21	54	3.0	464	10	US-09-918-995-15177	Sequence 15177, A
C 22	52.8	3.0	263	9	US-09-867-701-9696	Sequence 9696, Ap
23	52.8	3.0	476	10	US-09-854-867-118	Sequence 118, App
24	52.8	3.0	476	22	US-10-786-970A-118	Sequence 118, App
25	50	2.8	371	10	US-09-918-995-24284	Sequence 24284, A
C 26	50	2.8	446	9	US-09-880-107-1518	Sequence 1518, Ap
27	50	2.8	7093	16	US-10-101-510-527	Sequence 527, App
28	50	2.8	10126	18	US-10-242-355-1024	Sequence 1024, Ap
29	49.6	2.8	7140	22	US-10-211-028-3	Sequence 3, Appl
30	49.6	2.8	90597	22	US-10-211-028-1	Sequence 1, Appl
31	49.2	2.8	18535	9	US-09-764-878-385	Sequence 385, App
32	49.2	2.8	18535	15	US-10-079-854-385	Sequence 385, App
33	48	2.7	2463	14	US-10-027-632-102953	Sequence 102953, A
34	48	2.7	2463	18	US-10-027-632-102953	Sequence 102953, A
C 35	48	2.7	2927	24	US-10-450-763-24335	Sequence 24335, A
36	47.6	2.7	5430	24	US-11-097-143-14315	Sequence 14315, A
37	47.2	2.6	2227	26	US-11-097-143-14314	Sequence 14314, A
38	47.2	2.6	4602	26	US-11-097-143-14314	Sequence 14314, A
C 39	46.6	2.6	473	13	US-09-925-065A-844196	Sequence 844196, A
C 40	44.4	2.5	505	14	US-10-027-632-276057	Sequence 276057, A
C 41	44.4	2.5	505	18	US-10-027-632-276057	Sequence 276057, A
C 42	44	2.5	4216	20	US-10-437-963-53652	Sequence 53652, A
C 43	43.8	2.5	1599	20	US-10-437-963-2771	Sequence 2771, Ap
C 44	43.2	2.4	505	14	US-10-027-632-276059	Sequence 276059, A
C 45	43.2	2.4	505	18	US-10-027-632-276059	Sequence 276059, A

ALIGNMENTS

RESULT 1
US-09-563-817-201
; Sequence 201, Application US/09563817
; Patent No. US20020095031A1
; GENERAL INFORMATION:
; APPLICANT: Nehls, Michael C.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020095031A1 Human Polynucleotides and the
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: LEX-0021-USA
; CURRENT APPLICATION NUMBER: US/09/563,817
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: US 60/132,343
; PRIOR FILING DATE: 1999-05-04
; NUMBER OF SEQ ID NOS: 1008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 201
; LENGTH: 280
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(280)
; OTHER INFORMATION: n = A,T,C or G
US-09-563-817-201

Query Match 15.5% ; Score 275.8 ; DB 9 ; Length 280 ;


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; ORGANISM: Homo sapiens
; FEATURE:
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; OTHER INFORMATION: EXPRESSED IN ADULT LIVER. SIGNAL = 1.1
; OTHER INFORMATION: SWISSPROT HIT: O14197, EVALUE 2.10e-01
; OTHER INFORMATION: NT HIT: G14779172, EVALUE 0.00e+00
; OTHER INFORMATION: EST_HUMAN HIT: BF975008.1, EVALUE 0.00e+00
US-10-029-386-22242

Query Match      12.6%; Score 224.8; DB 17; Length 284;
Best Local Similarity 96.0%; Pred. No. 9.2e-59;
Matches 242; Conservative 0; Mismatches 7; Indels 3; Gaps 1;

QY 500 GTCTGAATCTCATACTCTTTGCGATTAACTGCAACAAAGGATTTCGAACGGGAGAGTA 559
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QY 560 AGTTTGTCCACACCGTTTCAGACCTCTTAAAGGAGTCAACGACAGACGTGACCTCTTGC 619
DB 224 AGTTTGTCCACACCGTTTCAGACCTCTTAAAGGAGTCAACGACAGATGTA---CCTTGC 168

QY 620 TGAAGGAGTCCACGACGAGGAGTGACGACCTGTTTCAAGGAGATCACAGCCTCTCTGCG 679
DB 167 TGAAGGAGTCCACGACGAGGAGTGACGACGCTGTTTCAAGGAGATCACAGCCTCTCTGCG 108

QY 680 TCTCCATCTCATCAAAACCTGAAACGAGGACCGACCTTGCCTGTGCTGCCAGGAATG 739
DB 107 TCTCCATCTCATCAAAACCTGAAACGAGGACCGACCTTGCCTGTGCTGCCAGGAATG 48

QY 740 TCAGTGTCTGATG 751
DB 47 TCAGTGTCTGATG 36

RESULT 5
US-10-450-763-28004
; Sequence 28004, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 28004
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (318)..(461)
; OTHER INFORMATION: 66% homologous to Homo sapiens Partial sequence of the clone
; OTHER INFORMATION: 9 protein, accession number W42400, Smith-Waterman Score=124.
US-10-450-763-28004

Query Match      11.6%; Score 207.6; DB 24; Length 463;
Best Local Similarity 93.9%; Pred. No. 2.6e-53;
Matches 216; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1219 GGCGTGGGCTCTACAGCCAGCAGATGCCCCCTCGAGAGCCTGGAGAACGGGACAGGA 1278
DB 234 GTCTCAGCCCTGGCTGAACAAAAGATGCCCCCTCGAGAGCCTGGAGAACGGGACAGGA 293

; LENGTH: 284
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR16.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER. SIGNAL = 1.1
; OTHER INFORMATION: SWISSPROT HIT: O14197, EVALUE 2.10e-01
; OTHER INFORMATION: NT HIT: G14779172, EVALUE 0.00e+00
; OTHER INFORMATION: EST_HUMAN HIT: BF975008.1, EVALUE 0.00e+00
US-10-029-386-22242

Query Match      12.6%; Score 224.8; DB 17; Length 284;
Best Local Similarity 96.0%; Pred. No. 9.2e-59;
Matches 242; Conservative 0; Mismatches 7; Indels 3; Gaps 1;

QY 500 GTCTGAATCTCATACTCTTTGCGATTAACTGCAACAAAGGATTTCGAACGGGAGAGTA 559
DB 284 GTCCGAATCTCATACTCTTTGCGATTAACTGCAACAAAGGATTTCGAACGGGAGAGTA 225

QY 560 AGTTTGTCCACACCGTTTCAGACCTCTTAAAGGAGTCAACGACAGACGTGACCTCTTGC 619
DB 224 AGTTTGTCCACACCGTTTCAGACCTCTTAAAGGAGTCAACGACAGATGTA---CCTTGC 168

QY 620 TGAAGGAGTCCACGACGAGGAGTGACGACCTGTTTCAAGGAGATCACAGCCTCTCTGCG 679
DB 167 TGAAGGAGTCCACGACGAGGAGTGACGACGCTGTTTCAAGGAGATCACAGCCTCTCTGCG 108

QY 680 TCTCCATCTCATCAAAACCTGAAACGAGGACCGACCTTGCCTGTGCTGCCAGGAATG 739
DB 107 TCTCCATCTCATCAAAACCTGAAACGAGGACCGACCTTGCCTGTGCTGCCAGGAATG 48

QY 740 TCAGTGTCTGATG 751
DB 47 TCAGTGTCTGATG 36

RESULT 6
US-11-060-756-3234
; Sequence 3234, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3234
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-060-756-3234

Query Match      11.6%; Score 206.8; DB 26; Length 465;
Best Local Similarity 94.5%; Pred. No. 4.6e-53;
Matches 225; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 274 GAGGTCTCTCAACAAAGCAGCAGCTGC-AGCGCTTCTACTCCTCGCCACATCGCCTCAGA 332
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QY 333 CGTGGCGCGGGTGGCGCTGGCTGGCTGCGCTCAACGAACACTCCCTGGAGCGCTA 392
DB 159 CGTGGCGTGGCGCGCGCTGGCTGGCTGCGCTCAACGAACACTCCCTGGAGCTA 218

QY 393 CTTGCACATGCTCTCTGGCCGACCGCTGACGCTGAGACATTTTATGAAGACTGGTCTTT 452
DB 219 CTTGCACATGCTCTCTGGCCGACCGCTGACGCTGAGCTACTTTTATGAAGACTGGTCTTT 278

QY 453 TGTGATGGATGAAGAAAGGTCAGATGCTTCTTACCATGGCAGCAGGTCTTGAATCC 510
DB 279 TGTGATGGATGAAGAGAGGTCAGATGCTTCTTACCATGGCAGCAGGTCTGAGGAGGCC 336

RESULT 7
US-11-060-756-7506
; Sequence 7506, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7506
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-060-756-7506
```

```
Query Match      11.6%; Score 206.8; DB 26; Length 465;
Best Local Similarity 94.5%; Pred. No. 4.6e-53;
Matches 225; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 274 GAGGTCTCAACAAGCAGGCTGC-AGCGCTTCTACTCCCTGCGCCACATCGCCTCAGA 332
    |||||
Db 99 GAGGTCTCAACAAGCAGGCTGC-AGCGCTTCTACTCCCTGCGCCACATCGCCTCAGA 158
    |||||
QY 333 CGTGGCCGGGGTGGCGCTGGCTGGCTGTGCGCTTCAACGAACACTCCCTGGAGCGCTA 392
    |||||
Db 159 CGTGGCTGGGCGCGCTGGCTGGCTGTGCGCTTCAACGAACACTCCCTGGAGTCTA 218
    |||||
QY 393 CTGACATGCTCTCTGGCGCAGCGCTGCAGGCTGAGCACTTTTATGAAGACTGGTCTTT 452
    |||||
Db 219 CTGACATGCTCTCTGGCGCAGCGCTGCAGGCTGAGTACTTTTATGAAGACTGGTCTTT 278
    |||||
QY 453 TGTGATGGATGAAGAAAGTCCAGTATGCTTCTACCATGGCAGCAGGTCTGAATCC 510
    |||||
Db 279 TGTGATGGATGAAGAGGTCCAGTATGCTTCTACCATGGCAGCAGGTGAGGAGGCC 336
    |||||
```

RESULT 8

```
US-09-925-065A-383678/c
; Sequence 383678, Application US/09925065A
; Publication No. US20050228172A9
```

```
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
```

```
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 10827.135
```

```
; CURRENT APPLICATION NUMBER: US/09/925, 065A
; CURRENT FILING DATE: 2001-08-08
```

```
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
```

```
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
```

```
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
```

```
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
```

```
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
```

```
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FASTSEQ for Windows Version 4.0
```

```
; SEQ ID NO 383678
; LENGTH: 492
```

```
; TYPE: DNA
; ORGANISM: Homo sapiens
```

```
US-09-925-065A-383678
```

```
Query Match      8.1%; Score 143.8; DB 13; Length 492;
Best Local Similarity 98.1%; Pred. No. 1.9e-33;
Matches 156; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
```

```
QY 1589 TGCCAGCTATCTTGGTATTTGTGAGGAGATCTAACCCACGTCGAGAACCATGTGGT 1648
    |||||
Db 158 TTGGCAGCTATCTTGGTATTTGTGAGGAGATCTAACCCACGTCGAGAACCATGTGGT 99
    |||||
```

```
QY 1649 GGAGAAATGGAGGAGAGAGAAATCCAAAGTTCTCTGATAGTCTCATTTGAGCTCTCTGGA 1708
    |||||
Db 98 GGAGAAATGGAGGAGAGAGAAAT-CAACAGTTCTCTGATAGTCTCATTTGAGCTCTCTGGA 40
    |||||
```

```
QY 1709 TCAGTCTTTCTTCAAGCTGTGTTTCTCTGGACTTTTC 1747
    |||||
Db 39 TCCAGTCTTTCTTCAAGCTGTGTTTCTCTGGACTTTTC 1
    |||||
```

RESULT 9

```
US-10-450-763-9353/c
; Sequence 9353, Application US/10450763
; Publication No. US20050196754A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
```

```
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
```

```
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
```

```
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 8336
; LENGTH: 500
```

```
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR16.3
```

```
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
```

```
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 9353
; LENGTH: 474
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (369)..(133)
; OTHER INFORMATION: 67% homologous to Homo sapiens Partial sequence of the clone
; OTHER INFORMATION: 9 protein, accession number W42400, Smith-Waterman Score=227.
US-10-450-763-9353
```

```
Query Match      7.6%; Score 135.4; DB 24; Length 474;
Best Local Similarity 72.6%; Pred. No. 7.5e-31;
Matches 175; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
```

```
QY 81 CTTTGAGGGAGAGAGATTGCCCTCGGATTCGACAGCAGGGTCCACCTGTCTGTGTGC 140
    |||||
Db 367 CTCTGCCAGAGCAGAGAAAGTTCTGACCACTGGCAGAGGGTCACTGTCTGTGTGC 308
    |||||
```

```
QY 141 CCAGTTTGAAGCGCTCTCGCATGGCTTGAAGAGAGTTCGAGGATTCGAGTTCGACTCAGC 200
    |||||
Db 307 CCAGTTTGAAGCGCTCTCGCATGGCTTGAAGAGAGTTCGAGGATTCGACTCAGC 248
    |||||
```

```
QY 201 GCAGCGATCAAGCAGGCGCGCTTTCGCCAGCAAAACCGAAACAGAGCCCGTGTCTG 260
    |||||
Db 247 GCAGCGATCAAGCAGGCGCGCTTTCGCCAGCAAAACCGAAACAGAGTGAAGTTCGCGCA 188
    |||||
```

```
QY 261 GTACTACGTGAAGAGGTCCTCAACAGCAGAGTCGAGCGCTTCTACTCCCTGCGCCA 320
    |||||
Db 187 GGCCACTGTGGCATGATGAACAGAGGATGAGCTGGAGGAGGAGACAGCCCTGGTGA 128
    |||||
```

```
QY 321 C 321
    |
Db 127 C 127
    |
```

RESULT 10

```
US-10-029-386-8336
```

```
; Sequence 8336, Application US/10029386
; Publication No. US20030194704A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
```

```
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
```

```
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
```

```
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 8336
; LENGTH: 500
```

```
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR16.3
```

```
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
```


OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3
OTHER INFORMATION: SWISSPROT HIT: Q92883, EVALUE 1.20e+00
OTHER INFORMATION: NT HIT: g115315787, EVALUE 2.00e-65
OTHER INFORMATION: EST_HUMAN HIT: AL135642.1, EVALUE 2.00e-65
US-10-029-386-8336

Query Match 7.2%; Score 128; DB 17; Length 500;
Best Local Similarity 100.0%; Pred. No. 1.5e-28;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 120 CAGGTCACCTCTGTGTGCCAGTTTGAAGCCGTCCTGCAGCATGGCTTGAAGAGGAG 179
Db |||||||
Qy 341 CAGGTCACCTCTGTGTGCCAGTTTGAAGCCGTCCTGCAGCATGGCTTGAAGAGGAG 400
Db |||||||
Qy 180 TCGAGGATTGGCACTCACAGCGGCAGCGATCAAGCAGCAGCGGCTTTGCCAGCAAAAC 239
Db |||||||
Qy 401 TCGAGGATTGGCACTCACAGCGGCAGCGATCAAGCAGCAGCGGCTTTGCCAGCAAAAC 460
Db |||||||
Qy 240 CGAAACAG 247
Db |||||||
Qy 461 CGAAACAG 468
Db |||||||

RESULT 11

US-10-029-386-22036
Sequence 22036, Application US/10029386
Publication No. US20030194704A1

GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
FILE REFERENCE: ASOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
SEQ ID NO 22036
LENGTH: 124
TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:
OTHER INFORMATION: MAP TO CHR16.3
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3
OTHER INFORMATION: NT HIT: g115315787, EVALUE 9.00e-64
OTHER INFORMATION: EST_HUMAN HIT: AL135642.1, EVALUE 1.00e-63
OTHER INFORMATION: SWISSPROT HIT: Q9SKU1, EVALUE 6.00e+00
US-10-029-386-22036

Query Match 7.0%; Score 124; DB 17; Length 124;
Best Local Similarity 100.0%; Pred. No. 1.3e-27;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 124 GTACCTCTGTGTGCCAGTTTGAAGCCGTCCTGCAGCATGGCTTGAAGAGGAGTCGA 183
Db |||||||
Qy 1 GTACCTCTGTGTGTGCCAGTTTGAAGCCGTCCTGCAGCATGGCTTGAAGAGGAGTCGA 60
Db |||||||
Qy 184 GGATTGGCACTCACAGCGGCAGCGATCAAGCAGCAGCGGCTTTGCCAGCAAAACCGAA 243
Db |||||||
Qy 61 GGATTGGCACTCACAGCGGCAGCGATCAAGCAGCAGCGGCTTTGCCAGCAAAACCGAA 120
Db |||||||
Qy 244 ACAG 247
Db |||||||
Qy 121 ACAG 124
Db |||||||

RESULT 12

Query Match 4.2%; Score 75; DB 13; Length 633;
Best Local Similarity 100.0%; Pred. No. 5.2e-12;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-10-450-763-215/c
Sequence 215, Application US/10450763
Publication No. US20050196754A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 215
LENGTH: 911
TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:
NAME/KEY: SIMILAR
LOCATION: (173)..(57)
OTHER INFORMATION: 100% homologous to Homo sapiens Partial sequence of the clone
OTHER INFORMATION: 9 protein, accession number W42400.Smith-Waterman Score=193.
US-10-450-763-215

Query Match 6.7%; Score 119; DB 24; Length 911;
Best Local Similarity 100.0%; Pred. No. 1.3e-25;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 129 CTGTCTGTGTGCCAGTTTGAAGCCGTCCTGCAGCATGGCTTGAAGAGGAGTCGAGGATT 188
Db |||||||
Qy 174 CTGTCTGTGTGCCAGTTTGAAGCCGTCCTGCAGCATGGCTTGAAGAGGAGTCGAGGATT 115
Db |||||||
Qy 189 GGCACCTCACAGCGGCAGCGATCAAGCAGCAGCGGCTTTGCCAGCAAAACCGAAACAG 247
Db |||||||
Qy 114 GGCACCTCACAGCGGCAGCGATCAAGCAGCAGCGGCTTTGCCAGCAAAACCGAAACAG 56
Db |||||||

RESULT 13

US-09-925-065A-681221
Sequence 681221, Application US/09925065A
Publication No. US20050238172A9

GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 681221
LENGTH: 633
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-681221

QY 427 AGCACTTTTATGAGACCTGGTCTTTTGTGATGGATGAAGAAAGGTCCAGTATGCTTCT 486
Db 484 AGCACTTTTATGAGACCTGGTCTTTTGTGATGGATGAAGAAAGGTCCAGTATGCTTCT 543
QY 487 ACCATGGCAGCAGGT 501
Db 544 ACCATGGCAGCAGGT 558

RESULT 14

US-11-097-143-11288
; Sequence 11288, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11288
; LENGTH: 1796
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-11288

Query Match 3.7%; Score 66.8; DB 26; Length 1796;
Best Local Similarity 49.4%; Pred. No. 3.1e-09;
Matches 173; Conservative 0; Mismatches 177; Indels 0; Gaps 0;
QY 233 GCAGAACCGAAGCAGAGCCGCTGTTCTGTGTAAGAGAGGTCTTCAACAAGCAGC 292
Db 396 GCAGAACCAACAATGACGCCACTTTCTGGGAATCTGCCAGACGCAATTTGACGCCCCACG 455
QY 293 AGCTGCAGCGCTTCTACTCCCTGGGCCACATCGCTCAGACGTGGCGGGGTGCGCCT 352
Db 456 AACCTCAGAGGTATATGGACCTTTAAGCAGATCTGGACGAATGTGGCAGAGCAGTGCCT 515
QY 353 GGCTGGCTGTGCGCTTCAAGAACACTCCCTGGAGCGCTACCTGCACATGCTCTGGCCG 412
Db 516 TCATACCGGCCCACTGAACAGAGCACTGCATAGCCATGTCTCACCTGGCTGAGCG 575
QY 413 ACCGCTGACGCTGAGCAGCTTTTATGAAGACTGGTCTTTGTGATGGATGAAGAAAGGT 472
Db 576 ACAGGAGCAGCTGCATCGATTTTACACACTTGGTCCCTGCTACTCAACGATGAGCGG 635
QY 473 CCAGTATGCTTCTTACCATCGCAGCGTCTGAACTCCATCTCTTTGCGATTAACATCG 532
Db 636 CCAGAGAGCTGCCAGAGATCGTAGACTCCCTCAGTGTACTGTTCGCCCTCAATGCG 695
QY 533 ACACAGAGGATTTGAACGGGCAGAGTAAGTTTGTCTCCACCGTTTCAGAC 582

Db 696 ACACCACTGAGCTTAATGCACCCAGGAGTCGACCCCAAGTGTTCGCCGTC 745

RESULT 15

US-11-097-143-11287/c
; Sequence 11287, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11287
; LENGTH: 3796
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-11287

Query Match 3.7%; Score 66.8; DB 26; Length 3796;
Best Local Similarity 49.4%; Pred. No. 4.5e-09;
Matches 173; Conservative 0; Mismatches 177; Indels 0; Gaps 0;
QY 233 GCAGAACCGAAGCAGAGCCGCTGTTCTGTGTAAGAGAGGTCTTCAACAAGCAGC 292
Db 2401 GCAGAACCAACAATGACGCCACTTTCTGGGAATTTGCCAGACGCAATTTGACGCCCCACG 2342
QY 293 AGCTGCAGCGCTTCTACTCCCTGGGCCACATCGCTCAGACGTGGCGGGGTGCGCCT 352
Db 2341 AAGCTCAGAGGTATATGGACCTTTAAGCAGATCTGGAGGAATGTGGCAGAGAGCTGCCT 2282
QY 353 GGCTGGCTGTGCGCTTCAAGAACACTCCCTGGAGCGCTACCTGCACATGCTCTGGCCG 412
Db 2281 TCATACCGGCCCACTGAACAGAGCACTGCATAGCCATGTCTCACCTGGCTGAGCG 2222
QY 413 ACCGCTGACGCTGAGCAGCTTTTATGAAGACTGGTCTTTGTGATGGATGAAGAAAGGT 472
Db 2221 ACAGGAGCAGCTGCATCGATTTTACACACTTGGTCCCTGCTACTCAACGATGAGCGG 2162
QY 473 CCAGTATGCTTCTTACCATGGCAGCAGGTCTGAACTCCATCTCTTTGCGATTAACATCG 532
Db 2161 CCAGAGAGCTGCCAGAGATCGTAGACTCCCTCAGTGTACTGTTCGCCCTCAATGCG 2102
QY 533 ACACAGAGGATTTGAACGGGCAGAGTAAGTTTGTCTCCACCGTTTCAGAC 582
Db 2101 ACACCACTGAGCTTAATGCACCCAGGAGTCGACCGCAAGTGTTCGCCGTC 2052

Search completed: October 26, 2005, 01:43:40
Job time : 1484 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 25, 2005, 18:28:14 ; Search time 286 Seconds
(without alignments)
10195.263 Million cell updates/sec

Title: US-10-070-255-4
Perfect score: 1782
Sequence: 1 atgagcgatcacagacaa.....taaatgtcttcattccttg 1782

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	133.4	7.5	190	4	US-09-513-999C-16002
2	66.8	3.7	811	4	US-09-270-767-12402
3	56.8	3.2	7218	1	US-08-232-463-14
4	54.4	3.1	36731	4	US-09-949-016-13770
5	54	3.0	601	4	US-09-949-016-13770
6	52.8	3.0	476	4	US-09-573-080A-118
7	52.2	2.9	961	4	US-09-976-594-221
8	49.6	2.8	9811	4	US-08-949-016-12759
9	47	2.6	100	4	US-09-513-999C-16212
10	46.8	2.6	60276	4	US-09-949-016-15004
11	46.8	2.6	60338	4	US-09-949-016-15094
12	46.8	2.6	94133	4	US-09-949-016-11901
13	46.8	2.6	94133	4	US-09-949-016-12713
14	46.8	2.6	94135	4	US-09-949-016-15934
15	46.8	2.6	94135	4	US-09-949-016-15936
16	46.8	2.6	94135	4	US-09-949-016-15937
17	46.8	2.6	94135	4	US-09-949-016-15937
18	44.8	2.5	474	4	US-09-621-976-18033
19	43.2	2.4	1002	4	US-09-902-540-8383
20	43.2	2.4	7035	4	US-08-902-540-878
21	43.2	2.4	23802	4	US-09-949-016-12107
22	43.2	2.4	23803	4	US-09-949-016-15878
23	43	2.4	1304	4	US-09-902-540-2596
24	43	2.4	16584	4	US-09-902-540-1119
25	42	2.4	23417	4	US-09-902-540-1207
26	41.4	2.3	505	4	US-09-621-976-15639
27	41.2	2.3	1926	3	US-09-249-585A-2

28	41.2	2.3	1926	4	US-09-410-399-3	Sequence 3, Appli
29	41.2	2.3	2580	3	US-09-050-863-2	Sequence 2, Appli
30	41.2	2.3	2580	3	US-09-359-081-2	Sequence 2, Appli
c 31	41.2	2.3	5452	2	US-09-130-114-1	Sequence 1, Appli
c 32	41.2	2.3	8705	4	US-09-647-344A-14	Sequence 14, Appli
33	41.2	2.3	9600	3	US-08-910-647-1	Sequence 1, Appli
34	41.2	2.3	9600	3	US-09-620-925-1	Sequence 1, Appli
35	41.2	2.3	10596	1	US-07-884-811-15	Sequence 15, Appli
36	41.2	2.3	10596	1	US-07-885-971-15	Sequence 15, Appli
37	41.2	2.3	10596	1	US-08-087-783A-15	Sequence 15, Appli
38	41.2	2.3	10596	1	US-08-194-088B-15	Sequence 15, Appli
39	41.2	2.3	10596	2	US-08-194-087-15	Sequence 15, Appli
40	41.2	2.3	10596	5	PCT-US93-04648-15	Sequence 15, Appli
c 41	41.2	2.3	16080	4	US-09-724-566A-48	Sequence 48, Appli
c 42	41.2	2.3	16080	4	US-09-471-669A-48	Sequence 48, Appli
43	41	2.3	1275	4	US-09-252-991A-251	Sequence 251, App
c 44	41	2.3	1785	4	US-09-252-991A-251	Sequence 281, App
45	40.6	2.3	1132	3	US-09-370-838-256	Sequence 256, App

ALIGNMENTS

RESULT 1

US-09-513-999C-16002
; Sequence 16002, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 16002
; LENGTH: 190
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-16002

Query Match	7.5%	Score 133.4;	DB 4;	Length 190;
Best Local Similarity	99.3%	Pred. No. 8.4e-26;		
Matches 134;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Oy	1464	CAGATCACTGCGAAACCTGCTCGACGGTGAGATGGAGCAGCTCAGCGGGCTCCGGCAAGA	1523	
Db	19	CAGATCACTGCGAAACCTGCTCGACGGTGAGATGGAGCAGCTCAGCGGGCTCCGGCAAGA	78	
Oy	1524	GGTGGACACCTTGAAGAGGAGGTGGCTGAACAGGAGGAGCGGAGGCATGAAGGTCCA	1583	
Db	79	GGTGGACACCTTGAAGAGGAGGTGGCTGAACAGGAGGAGCGGAGGCATGAAGGTCCA	138	
Oy	1584	GGCGCTGGCCAGCTA	1598	
Db	139	GGCGCTGGCCAGGTA	153	

RESULT 2

US-09-270-767-12402
; Sequence 12402, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17

```

; ; NUMBER OF SEQ ID NOS: 62517
; ; SOFTWARE: PatentIn Ver. 2.0
; ; SEQ ID NO 12402
; ; LENGTH: 811
; ; TYPE: DNA
; ; ORGANISM: Drosophila melan
US-09-270-767-12402

```

Query Match 3.7%; Score 66.8; DB 4; Length 811;
Best Local Similarity 49.4%; Pred. NO. 1e-07;
Matches 173; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

RESULT 3

US-08-232-463-14/c
; Sequence 14, Application US/08232463

```

; Patent No. 5670367
;
; GENERAL INFORMATION:
;
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
;
; NUMBER OF SEQUENCES: 52
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA

```

```

; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
; US-08-232-463-14

      Query Match          3.2%;   Score 56.8;   DB 1;   Length 7218;
      Best Local Similarity 3.3%;   Pred. No. 0.00013;
      Matches 13;   Conservative 225;   Mismatches 152;   Indels 0;   Gaps 0;

QY      734  GGAATGTCAGTCTGATGCCAAATGCAAAAGAGCGGAGAAAGAAAGAAAGATGTACCA 793
      ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1439  GGTACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1380

QY      794  ACATAATCTCATTTGATGATGAGGAAGATCAGCAGAACTCTCGGGAGCGTGTAAAAAAGA 853
      ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1379  RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1320

QY      854  CACCTGGGCGAGGAGAGCTCAGAGACAACCTCCGACCGCTCTCTGTCAATATCATGT 913
      ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1319  RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1260

QY      914  CCGCCTTTGAAAGCCCTTCGCGCCTAACTCCAATGGAAGTCAGAGCAGCAACTCATGGA 973
      ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1259  RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1200

QY      974  AAATTGATCCCTGTCTTTGAAACGGGAGTTTGGGTACCAAGACGTGTGTAAGAAAGCA 1033
      ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1199  RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1140

QY      1034  TCGATGATGAAGATGTGATGAAACGAAGATCACGTGATGGAACACTCATCAGGAAGCA 1093
      ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1139  RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1080

QY      1094  AGCACAGGGGCCACTCGAGTCCCGCAGA 1123
      ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1079  RRRRRRRRRRRRRATCGCAAGCTCCCTCGA 1050
      ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 4

```

US-09-949-016-13770/C
; Sequence 13770, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13770
; LENGTH: 36731
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13770

```

REGISTRATION NUMBER: 237700
REFERENCE/DOCKET NUMBER: 30472/114 IMM
TELECOMMUNICATION INFORMATION:

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: repeat region
; LOCATION: (1)..(476)
; PUBLICATION INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS: Jurka, J; Wilchewicz, J; Milosavljevic, A
; TITLE: Prototypic sequences for human repetitive DNA
; JOURNAL: Journal of Molecular Evolution
; VOLUME: 35
; ISSUE: 4
; PAGES: 286-291
; DATE: 1992-10-
; DATABASE ACCESSION NUMBER: Database of repetitive elements (repbase)
; DATABASE ENTRY DATE:
; DATABASE ENTRY DATE: 1996-01-26
; US-09-573-080A-118

Query Match 3.0%; Score 52.8; DB 4; Length 476;
Best Local Similarity 69.8%; Pred. No. 0.00045;
Matches 88; Conservative 0; Mismatches 32; Indels 6; Gaps 1;

QY 1662 GAGAGAGAAATCAACAGATTCTCGATAGTCTCATTTGAGCTCCTGGATCCAGTCTTTTCCCT 1721
DB 313 GAGATGGAGAGACAGATTTCTCGATGACATCATTTTGAGCACCCTGGATCCAGCATCGCT 372

QY 1722 GAAG-----CTGTGTTTCTCTGGACTTTTTCATGTATGTGAGCCATAAATTCCTTTCA 1775
DB 373 GAAGCCAGATCTATGCTACCCCTGGACTTTTCAGTTACATGAGCCATAAATTCCTTTT 432

QY 1776 TTCCTT 1781
DB 433 TTGCTT 438

RESULT 7
US-09-976-594-221
; Sequence 221, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchsinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 221
; LENGTH: 961
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 330927.1
US-09-976-594-221

Query Match 2.9%; Score 52.2; DB 4; Length 961;
Best Local Similarity 71.1%; Pred. No. 0.0009;
Matches 69; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1679 GTCTCTGATAGTCTCATTTGAGCTCCTGGATCCAGTCTTTCCCTGAAGCTGTGTTCCCTCT 1738
DB 861 GTCTTTGGTGACATCTTTTGGAGCCACTAGACCAAGCTTTACCTGAAGCAGAGCTACCTCA 920

QY 1739 GGACTTTTCATGTATGTGAGCCCAATAAATTCGCTTTCA 1775
DB 921 GAACCTTTTCAGTATGTGAGCCCAATAAATTCGCTCA 957

RESULT 8

```

```
US-09-949-016-12759
; Sequence 12759, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12759
; LENGTH: 9811
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12759

Query Match 2.8%; Score 49.6; DB 4; Length 9811;
Best Local Similarity 61.7%; Pred. No. 0.013;
Matches 79; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 1654 AATGGAGGAGAGAGAAATCCACAGTTCCTGATAGTCTCATTTGAGCTCCTGGATCCAG 1713
DB 3752 AAGAAGAGAGTGTAGTGAGTGACCATTTCTTATTCATCCTTTGAGGCCCTACACCTAA 3811

QY 1714 TCCTTCCTGAAGCTGTGTTTCTCTGAGCTTTTCATGTATGTGAGCCAAATAATGCTTT 1773
DB 3812 TCATTCATGAAGCTATACCACTCCAGCCCTTTTCAATTACTTGAGCCAAATTCCTT 3871

QY 1774 CATTCCTT 1781
DB 3872 TAATAGTT 3879

RESULT 9
US-09-513-999C-16212
; Sequence 16212, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 16212
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 13
; OTHER INFORMATION: m=a or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 14
; OTHER INFORMATION: m=a or c
US-09-513-999C-16212

Query Match 2.6%; Score 47; DB 4; Length 100;
```

```
Best Local Similarity 100.0%; Pred. No. 0.0078;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGCGGATCAGAACAAATGACAAAGACAAATTTCTCTGGAGCG 47
DB 53 ATGAGCGGATCAGAACAAATGACAAAGACAAATTTCTCTGGAGCG 99

RESULT 10
US-09-949-016-15004/c
; Sequence 15004, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15004
; LENGTH: 60276
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(60276)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15004

Query Match 2.6%; Score 46.8; DB 4; Length 60276;
Best Local Similarity 73.2%; Pred. No. 0.17;
Matches 60; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1692 TCATTGAGCTCCTGGATCCAGTCTTTCTCTGAGCTGTGTTTCTCTGGACTTTTCATGT 1751
DB 10119 TCTTAGAGCACCTGATCCAGCCCTGCTGAGCCATCTACCCCTGGACTTCTCAGTT 10060

QY 1752 ATGTGAGCCAAATAAATGCTTT 1773
DB 10059 GTGTGAGCCAAGAATTGCTTT 10038

RESULT 11
US-09-949-016-15694/c
; Sequence 15694, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15694
; LENGTH: 60338
; TYPE: DNA
; ORGANISM: Human
```



```
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(60338)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15694

Query Match          2.6%; Score 46.8; DB 4; Length 60338;
Best Local Similarity 73.2%; Pred. No. 0.17;
Matches 60; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy 1692 TCATTGAGCTCCGATCCAGTCTTCTCGAAGCTGTGTTCTCTCGAGCTTTTCAGT 1751
Db 10181 TCTTAGAAGCACCTGGATCCAGCCCTGCTGAAGCCATCTACCCCTGGACTTCTCAGT 10122

Qy 1752 ATGTGAGCAATAAATGCTTT 1773
Db 10121 GTGTGAGCAAGAATTGCTTT 10100

RESULT 12
US-09-949-016-11901/c
; Sequence 11901, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11901
; LENGTH: 94133
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11901

Query Match          2.6%; Score 46.8; DB 4; Length 94133;
Best Local Similarity 67.3%; Pred. No. 0.21;
Matches 66; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 1678 AGTTCCTGATAGTCTCATTTGAGCTCCTGGATCCAGTCTTTCCTGAAGCTGTGTTTCCTC 1737
Db 40227 AGAGCTTGAGAACACAGTTTAAGCATTTGGAGTCAGCTATGCTTGAAGCCATGCTCCCTC 40168

Qy 1738 TGGACTTTTCATGTATGTGAGCCCAATAAATGCTTTCA 1775
Db 40167 TAGACTTTTCAGTTACATGAGCCCAATAAATATTTTAA 40130

RESULT 13
US-09-949-016-12713/c
; Sequence 12713, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
```

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; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12713
; LENGTH: 94133
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12713

Query Match          2.6%; Score 46.8; DB 4; Length 94133;
Best Local Similarity 67.3%; Pred. No. 0.21;
Matches 66; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 1678 AGTTCCTGATAGTCTCATTTGAGCTCCTGGATCCAGTCTTTCCTGAAGCTGTGTTTCCTC 1737
Db 40227 AGAGCTTGAGAACACAGTTTAAGCATTTGGAGTCAGCTATGCTTGAAGCCATGCTCCCTC 40168

Qy 1738 TGGACTTTTCATGTATGTGAGCCCAATAAATGCTTTCA 1775
Db 40167 TAGACTTTTCAGTTACATGAGCCCAATAAATATTTTAA 40130

RESULT 14
US-09-949-016-15934/c
; Sequence 15934, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15934
; LENGTH: 94135
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15934

Query Match          2.6%; Score 46.8; DB 4; Length 94135;
Best Local Similarity 67.3%; Pred. No. 0.21;
Matches 66; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 1678 AGTTCCTGATAGTCTCATTTGAGCTCCTGGATCCAGTCTTTCCTGAAGCTGTGTTTCCTC 1737
Db 40227 AGAGCTTGAGAACACAGTTTAAGCATTTGGAGTCAGCTATGCTTGAAGCCATGCTCCCTC 40168

Qy 1738 TGGACTTTTCATGTATGTGAGCCCAATAAATGCTTTCA 1775
Db 40167 TAGACTTTTCAGTTACATGAGCCCAATAAATATTTTAA 40130

RESULT 15
US-09-949-016-15935/c
; Sequence 15935, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
```

```
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 15935
; LENGTH: 94135
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15935
```

```
Query Match      2.6%; Score 46.8; DB 4; Length 94135;
Best Local Similarity 67.3%; Pred. No. 0.21;
Matches 66; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY      1678 AGTTCTGATAGTCTCATTTGAGCTCTCTGGATCCAGTCTTTCTCTGAAGCTGTGTTTCTTC 1737
Db      40227 AGACCTGAGAACACAGTTTAAGCATTTGGAGTCAGCTATGCCCTGAAGCCATGCTCCCTC 40168

QY      1738 TGGACTTTTCATGTATGTGAGCCCAATAAATTGCTTTCA 1775
Db      40167 TAGACTTTTCAGTTACATGAGCCCAATAAATAATTTTA 40130
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Search completed: October 25, 2005, 21:20:34
Job time : 289 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 25, 2005, 21:16:28 ; Search time 981 Seconds
(without alignments)
10753.292 Million cell updates/sec

Title: US-10-070-255-4
Perfect score: 1782
Sequence: 1 atgagcggatcacagacaa.....taaatgctttcattccttg 1782

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Desc04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1782	100.0	1782	4	AAD04333
2	1742	97.8	1906	2	AAV03323
3	1595	89.5	2873	4	AAD04335
4	1595	89.5	3139	4	AAD04334
5	1129.8	63.4	2248	4	AAH15665
6	816.8	45.8	6045	4	AAH18235
7	639.8	35.9	7330	4	AAH04973
8	364.2	20.4	33147	4	AAK67282
9	275.8	15.5	280	6	ABS72233
10	247	13.9	454	5	AAS64410
11	227.8	12.8	542	12	ACH75347
12	224.8	12.6	284	12	ACH89047
13	207.6	11.6	463	5	AAS92200
14	135.4	7.6	474	5	AAS73549
15	133.4	7.5	190	3	AAC11927
16	128	7.2	500	12	ACH75141
17	124	7.0	124	12	ACH88841
18	119	6.7	911	5	AAS64411
19	66.8	3.7	1796	4	ABL09365
20	66.8	3.7	3796	4	ABL09364

C	21	63.8	3.6	3931	4	ABA09172	Human BG3
C	22	59.6	3.3	214520	10	ADL13471	Adl13471 Osteoarthritis
	23	59	3.3	3927	10	ADP81729	Adf81729 Leukaemia
	24	58.4	3.3	595	13	ADOS3383	Adqs3383 Novel can
	25	54.4	3.1	813	5	AAS85362	Aas85362 DNA encod
	26	54	3.0	464	9	ACH27965	ACH27965 Human adu
C	27	52.8	3.0	263	6	ABL86718	ABL86718 Human ova
	28	51.8	3.0	476	7	ADS31085	Ads31085 Human gen
	29	52.2	2.9	729	10	ADE07225	Ade07225 Novel cod
	30	52.2	2.9	941	5	ABA21208	Aba21208 Human ner
	31	52.2	2.9	941	5	ABA21210	Aba21210 Human ner
	32	52.2	2.9	961	12	ADL12492	Adl12492 Human ste
	33	52.2	2.9	3916	13	ADR07577	Adr07577 Full leng
	34	51.8	2.9	617	5	ABA14117	Aba14117 Human ner
	35	50.2	2.8	2000	8	ADA71938	Ada71938 Rice gene
	36	50	2.8	371	9	ACH37072	Ach37072 Human end
C	37	50	2.8	446	6	ABN95020	Abn95020 Gene #151
C	38	50	2.8	769	4	AAI95747	Aai95747 Human neu
	39	50	2.8	5684	3	AAC59953	Aac59953 Human sec
	40	50	2.8	5684	8	ABZ73290	Abz73290 Secreted
	41	50	2.8	5684	10	ABZ66903	Abz66903 Human sec
	42	50	2.8	7093	6	ABZ35416	Abz35416 Human gen
	43	50	2.8	10126	4	AAI99260	Aai99260 Human exc
	44	50	2.8	10126	5	AAI63610	Aai63610 Human kid
	45	49.6	2.8	90597	10	ADJ72363	Adj72363 Streptomy

ALIGNMENTS

RESULT 1

AAD04333

ID AAD04333 standard; cDNA; 1782 BP.

XX AAD04333;

DT 04-JUL-2001 (first entry)

XX Human TNF receptor-associated factor (TRAF2) binding protein, IREN cDNA.

DE Human; Tumour Necrosis Factor; TNF; TNF Receptor Associated Factor;

XX TRAF2; TRAF2 binding protein; IREN; IkappaB Regulator; immunosuppressive;

KW nuclear factor-kappaB; NF-kappaB; cytostatic; tumour; AIDS;

KW acquired immune deficiency syndrome; rheumatic disease; apoptosis;

KW autoimmune disease; septic shock; graft-vs-host reaction; inflammation;

KW anorexia; anti-HIV; therapy; ss.

XX Homo sapiens.

OS Key

FT CDS

FT Location/Qualifiers

FT 1..1626

FT /*tag= a

FT /product= "Human TRAF2-binding protein, IREN"

XX WO200116314-A1.

XX 08-MAR-2001.

XX 31-AUG-2000; 2000WO-IL000517.

XX 02-SEP-1999; 99IL-00131719.

XX (YEDA) YEDA RES & DEV CO LTD.

XX Wallach D, Malinin N, Sinha I, Leu S;

XX WPI; 2001-281387/29.

XX P-PSDB; AAE00683.

XX New DNA sequence encoding Tumor Necrosis Factor receptor associated

PT factor (TRAF) binding proteins (IREN) for treatment or prevention of

PT pathological conditions associated with NF-kappaB induction.

XX

Claim 1; Fig 3B; 118bp; English.

The present cDNA sequence encodes human tumour necrosis factor (TNF) receptor-associated factor (TRAF2) binding protein, IREN. A fragment of this IREN molecule is capable of binding to TRAF2 protein at position 225 -501. The invention relates to human tumour necrosis factor (TNF) receptor-associated factor (TRAF2) binding protein designated as IREN (IkappaB Regulator), its isoforms IREN-10B, IREN-E and their corresponding cDNA molecules. IREN is useful for modulating/mediating the activity of transcription factor NF (Nuclear Factor)-kappaB or any other intracellular signalling activity mediated by TRAF2. IREN is useful in the prevention and treatment of a pathological condition associated with NF-kappaB induction (abnormal) e.g. AIDS (acquired immune deficiency syndrome), autoimmune diseases, tumours, rheumatic diseases, anorexia, septic shock and graft-vs-host reactions. IREN also plays an important role in the control of inflammation and other non-apoptotic effects of TNF as well as in the control of apoptosis. The invention also relates to method for screening, identifying and producing a molecule capable of modulating activities mediated by IREN. IREN antibodies are useful for the purification of new proteins from different sources, including cell extracts or transformed cell lines, in addition IREN can be used in diagnostic purposes for identifying disorders related to abnormal functioning of cellular effects mediated directly by TRAF proteins

Sequence 1782 BP; 456 A; 458 C; 504 G; 364 T; 0 U; 0 Other;

Query Match 100.0%; Score 1782; DB 4; Length 1782;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1782; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PS	1	ATGAGCGGATCACAGAACATGACAAAGACAATTTCTGCTGAGCGACTGCTGGATGCA	60
XX	1	ATGAGCGGATCACAGAACATGACAAAGACAATTTCTGCTGAGCGACTGCTGGATGCA	60
CC	61	GTGAAACAGTCCAGATCCCGTTTGGAGGGAGAAAGAGATTGCTCGGATTCGGACAGC	120
CC	61	GTGAAACAGTCCAGATCCCGTTTGGAGGGAGAAAGAGATTGCTCGGATTCGGACAGC	120
QY	121	AGGGTCACTGTCTGTGTCGCCAGTTTGAAGCCGTCCTGAGCATGGCTTTGAAGAGAGT	180
DB	121	AGGGTCACTGTCTGTGTCGCCAGTTTGAAGCCGTCCTGAGCATGGCTTTGAAGAGAGT	180
QY	181	CGAGGATTGGCACTCAGCGGGCAGCGATCAAGCAGCGCGGCTTTGCCAGCAAAACC	240
DB	181	CGAGGATTGGCACTCAGCGGGCAGCGATCAAGCAGCGCGGCTTTGCCAGCAAAACC	240
QY	241	GAACAGAGCCCTGTCTGTGTTACTACGTGAAGAGGTCTCAACAGCAGAGTGCAG	300
DB	241	GAACAGAGCCCTGTCTGTGTTACTACGTGAAGAGGTCTCTCAACAGCAGAGTGCAG	300
QY	301	CGCTTCTACTCCCTGCGCCACATCGCTCAGAGTGGCGCGGGTCCGCGCTGGCTGCGC	360
DB	301	CGCTTCTACTCCCTGCGCCACATCGCTCAGAGTGGCGCGGGTCCGCGCTGGCTGCGC	360
QY	361	TGTGCCCTCAACGAACACTCCCTGGAGCGCTACTGTCACATGCTCCTGGCCGACCGCTGC	420
DB	361	TGTGCCCTCAACGAACACTCCCTGGAGCGCTACTGTCACATGCTCCTGGCCGACCGCTGC	420
QY	421	AGGCTGAGCACTTTTATGAAGTCTGGTCTTTTGTGATGATGAAGAAAGGTCCAGTATG	480
DB	421	AGGCTGAGCACTTTTATGAAGTCTGGTCTTTTGTGATGATGAAGAAAGGTCCAGTATG	480
QY	481	CTTCTACCATGCGAGAGTCTGAACTCCATCTCTTTGCGATTAACTCGACACAG	540
DB	481	CTTCTACCATGCGAGAGTCTGAACTCCATCTCTTTGCGATTAACTCGACACAG	540
QY	541	GATTGAAACCGGCGAGAGTAAAGTTTGTCTCCACCGTTTCAGACCTCTTAAAGGAGTCAACG	600
DB	541	GATTGAAACCGGCGAGAGTAAAGTTTGTCTCCACCGTTTCAGACCTCTTAAAGGAGTCAACG	600
QY	601	CAGAACGTGACCTCTTCTGTAAGGAGTCCACGAAAGAGTGAAGAGCTGTTTCAGGGAG	660
DB	601	CAGAACGTGACCTCTTCTGTAAGGAGTCCACGAAAGAGTGAAGAGCTGTTTCAGGGAG	660

Qy 1741 ACTTTTCATGTATGTAGCCCAATTAATGCTTTTCATTCCTTG 1782
 Db |||||

RESULT 2

ID AAV03323 standard; cDNA; 1906 BP.
 XX
 AC AAV03323;

XX 15-APR-1998 (first entry)

XX 5' end of clone 9, which encodes a TRAF2 binding protein.

XX Human tumour necrosis factor receptor-associated factor 2; TRAF2;
 KW TRAF-2 binding protein; NF-kappaB activity; NF-kappaB induction;
 KW intracellular signalling activity; acute hepatitis;
 KW autoimmune-induced cell death; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH 94..1906
 CDS /*tag= a

FT /codon= 127-129, aa:Ser

FT /note= "no ATG start or STOP codon given"

XX W09737016-A1.

XX 09-OCT-1997.

XX 01-APR-1997; 97WO-IL000117.

XX 02-APR-1996; 96IL-00117800.

XX 26-AUG-1996; 96IL-00119133.

XX (YEDA) YEDA RES & DEV CO LTD.

XX Wallach D, Malinin N, Boldin M, Kovalenko A, Mett I;

XX WPI; 1997-503101/46.

XX P-PSDB; AAW42400.

XX DNA encoding tumour necrosis factor receptor-associated factor binding
 PT molecule - used for modulation or mediation in cells of the activity of
 PT NF-kB.

XX Claim 4; Fig 3; 127pp; English.

XX The present sequence represents the 5' end of clone 9, which encodes a
 CC TRAF2 binding protein. Clone 9 is a partial clone, which lacks most of
 CC its 5' end of the coding DNA sequence. A cDNA library prepared from B-
 CC cells was screened for proteins that associate with TRAF2, and the
 CC present sequence isolated. The clone 9 protein is capable of binding to
 CC at least amino acids 222-501 of TRAF2. The TRAF-2 binding proteins can be
 CC used for modulation or mediation in cells of the activity of NF-kappaB or
 CC any other intracellular signalling activity modulated or mediated by
 CC TRAF2. TRAF-binding proteins are especially used for prevention or
 CC treatment of pathological conditions associated with NF-kB induction,
 CC e.g. acute hepatitis, autoimmune-induced cell death, e.g. death of the
 CC beta Langerhans cells or the pancreas that results in diabetes, the death
 CC of cells in graft rejection, the death of oligodendrocytes in the brain
 CC in multiple sclerosis, and AIDS-inhibited T cell suicide which causes
 CC proliferation of the AIDS virus and hence the AIDS disease. The proteins
 CC are also useful for screening of ligands capable of binding to a protein,
 CC which are useful for modulating cellular activity modulated/mediated by
 CC TRAF2

XX Sequence 1906 BP; 482 A; 492 C; 547 G; 378 T; 0 U; 7 Other;

XX Query Match 97.8%; Score 1742; DB 2; Length 1906;

XX Best Local Similarity 99.6%; Pred. No. 0;

Matches 1775; Conservative 0; Mismatches 4; Indels 3; Gaps 3;
 Qy 1 ATGAGCGGATCACAGAACAAATGACAAAGACAAATTTCTGCTGGAGCCACTCTCGATGCA 60
 Db |||||
 Qy 118 ATGAGCGGATCNCNGAACNATGACAAAGACAAATTTCTGCTGGAGCCACTCTCGATGCA 177
 Db |||||
 Qy 61 GTGAAACAGTGCCAGATCCGCTTTGGAGGGAGAAAGAGATTGCTCGGATTCGACAGC 120
 Db |||||
 Qy 178 GTGAAACAGTGCCAGATCCGCTTTNGAGGGAGAAAGAGATTGCTCGGATTCGACAGC 237
 Db |||||
 Qy 121 AGGTCACCTGTCTGTGTGCCAGTTTGAAGCCGTCTCTGAGCATGCTTGAAGAGAGT 180
 Db |||||
 Qy 238 AGGTCACCTGTCTGTGTGCCAGTTTGAAGCCGTCTCTGAGCATGCTTGAAGAGAGT 297
 Db |||||
 Qy 181 CGAGGATTGGCACTCACAGCGGAGCGATCAAGCAGGACGCGGCTTTGCCAGCAAAACC 240
 Db |||||
 Qy 298 CGAGGATTGGCACTCACAGCGGAGCGATCAAGCAGGACGCGGCTTTGCCAGCAAAACC 357
 Db |||||
 Qy 241 GAAACAGAGCCGTTTCTGGTACTACGTGAAGAGGCTCTCAACAAGCAGAGCTCGAG 300
 Db |||||
 Qy 358 GAAACAGAGCCGTTTCTGGTACTACGTGAAGAGGCTCTCAACAAGCAGAGCTCGAG 417
 Db |||||
 Qy 301 CGCTTCTACTCCCTGCGCCACATCGCTCAGACGTGGCGCGGGTCTGGCCCTGGCTGGC 360
 Db |||||
 Qy 418 CGCTTCTACTCCCTGCGCCACATCGCTCAGACGTGGCGCGGGTCTGGCCCTGGCTGGC 477
 Db |||||
 Qy 361 TGTGCCCTCAACGAACACTCCCTGGAGCGCTTACCTGCACATGCTCTGGCGAGCCGCTGC 420
 Db |||||
 Qy 478 TGTGCCCTCAACGAACACTCCCTGGAGCGCTTACCTGCACATGCTCTGGCGAGCCGCTGC 537
 Db |||||
 Qy 421 AGGCTGAGCACTTTTATGAAGAGTGGTCTTTTGTGATGATGAAGAAAGTCCAGTATG 480
 Db |||||
 Qy 538 AGGCTGAGCACTTTTATGAAGAGTGGTCTTTTGTGATGATGAAGAAAGTCCAGTATG 597
 Db |||||
 Qy 481 CTTCTACCATGGCAGCAGGTCTGAACTCCATACTCTTTGGGATTAAATCGACAAACAG 540
 Db |||||
 Qy 598 CTTCTACCATGGCAGCAGGTCTGAACTCCATCTCTTTGCGATTAAATCGACAAACAG 657
 Db |||||
 Qy 541 GATTGAAACGGGACAGATAAGTTTGTCTCCACCCCTTTTTCAGACCTTTTAAAGAGTCAACG 600
 Db |||||
 Qy 658 GATTGAAACGGGACAGATAAGTTTGTCTCCACCCCTTTTTCAGACCTTTTAAAGAGTCAACG 717
 Db |||||
 Qy 601 CAGAACTGACCTCTCTGCTGAAAGAGTCCACGCAAGAGTGAGCAGCCCTGTTTCAGGGAG 660
 Db |||||
 Qy 718 CAGAACTGACCTCTCTGCTGAAAGAGTCCACGCAAGAGTGAGCAGCCCTGTTTCAGGGAG 777
 Db |||||
 Qy 661 ATCAGACCTCTCTGCTGCGCTCTCCATCTCATCAAACTGAAACAGGAGACGACCCCTTG 720
 Db |||||
 Qy 778 ATCAGACCTCTCTGCTGCGCTCTCCATCTCATCAAACTGAAACAGGAGACGGA-CCCTTG 836
 Db |||||
 Qy 721 CCTGTCGTGCCAGGAATGTCAGTGTGATGCCAAATGCAAAAGAGAGCGAAGAA 780
 Db |||||
 Qy 837 CCTGTCGTGCCAGGAATGTCAGTGTGATGCCAAATGCAAAAGAGAGCGGAAGAA 896
 Db |||||
 Qy 781 AAGAAAGTGACCAACATAATCTCATTTGATGATGAGGAAGATGAGCAGAACTCTGGGGAC 840
 Db |||||
 Qy 897 AAGAAAGTGACCAACATAATCTCATTTGATGATGAGGAAGATGAGCAGAACTCTGGGGAC 956
 Db |||||
 Qy 841 GTGTTTAAAAGACACCTCTGGGCGAGGAGAGCTCAGAGCAACTCGGACCGCTCTCT 900
 Db |||||
 Qy 957 GTGTTTAAAAGACACCTCTGGGCGAGGAGAGCTCAGAGGACAACTCGGACCGCTCTCT 1016
 Db |||||
 Qy 901 GTCAATATCATGTCCGCTTTTAAAAGCCCTTTGGGGCTTAACCTCAATGAAGTTCAGAGC 960
 Db |||||
 Qy 1017 GTCAATATCATGTCCGCTTTTAAAAGCCCTTTGGGGCTTAACCTCAATGNA-TCAGAGC 1075
 Db |||||
 Qy 961 AGCAACTCATGGAATAATTTGATTCCTCTCTTTGAAACCGGGAGTTTGGGTACCAAGACT 1020
 Db |||||
 Qy 1076 AGCAACTCATGGAATAATTTGATTCCTCTCTTTGAAACCGGGAGTTTGGGTACCAAGACT 1135
 Db |||||
 Qy 1021 GATGTGAAAAGCATCGATGATGAAGATGATGATGATGATGATGATGATGATGATGATGATG 1080
 Db |||||
 Qy 1136 GATGTGAAAAGCATCGATGATGAAGATGATGATGATGATGATGATGATGATGATGATGATG 1195
 Db |||||

QY 1081 TCATCAGGAAGNAGACACAGGGGCCACTCGAGTCCGCCGAGNAGCCACTGGNAGGAAAC 1140
 Db 1196 TCATCAGGAAGNAGACACAGGGGCCACTCGAGTCCGCCGAGNAGCCACTGGNAGGAAAC 1255
 QY 1141 ACCTGCTCTCCAGATGACACAGCTGGGCTCCGCTCAAGGTGCTGACAAATGACTCCGAC 1200
 Db 1256 ACCTGCTCTCCAGATGACACAGCTGGGCTCCGCTCAAGGTGCTGACAAATGACTCCGAC 1315
 QY 1201 ATCTCTTCTCCCTGCTAGTGGCGTGGCTCTACAGCCGACAGATGCCCCCTCGAAGC 1260
 Db 1316 ATCTCTTCTCCCTGCTAGTGGCGTGGCTCTACAGCCGACAGATGCCCCCTCGAAGC 1375
 QY 1261 CTGGAGACGGGACAGACAGAGGACCAAGTCTCCCGATCCCTGGACTTCGGTACAGT 1320
 Db 1376 CTGGAGACGGGACAGACAGAGGACCAAGTCTCCCGATCCCTGGACTTCGGTACAGT 1435
 QY 1321 GTGGAAGCCAGCTCTCCAGGCCACGAAGTCCCTCTGAGCAGCCTGTACCTTCTGCTCA 1380
 Db 1436 GTGGAAGCCAGCTCTCCAGGCCACGAAGTCCCTCTGAGCAGCCTGTACCTTCTGCTCA 1494
 QY 1381 GTGCCAGAGTCCATGACAAATTAGTGAATCGCCGACGCCCACTGTGCCATGATGAACAG 1440
 Db 1495 GTGCCAGAGTCCATGACAAATTAGTGAATCGCCGACGCCCACTGTGCCATGATGAACAG 1554
 QY 1441 AAGGATGAGCTGGAGGAGGACAGATCACTGCGAACTGCTGACCGTGGATGGAG 1500
 Db 1555 AAGGATGAGCTGGAGGAGGAGAACAGATCACTGCGAACTGCTGACCGTGGATGGAG 1614
 QY 1501 CACTCAGCCGCGCTCCGGCAAGAGGTGGACACCTTGAAAAGGAGGTGGCTGAACAGGAG 1560
 Db 1615 CACTCAGCCGCGCTCCGGCAAGAGGTGGACACCTTGAAAAGGAGGTGGCTGAACAGGAG 1674
 QY 1561 GAGCGCAGGCGATGAAGTCCAGGCGCTGGCCAGCTATCTTTGCTATTTTGTGAGGAGA 1620
 Db 1675 GAGCGCAGGCGATGAAGTCCAGGCGCTGGCCAGCTATCTTTGCTATTTTGTGAGGAGA 1734
 QY 1621 TTCTACCCACGCTGAGACCACTGCTGGAGAAATGGAGGAGAGAAATCCACAGT 1680
 Db 1735 TTCTACCCACGCTGAGACCACTGCTGGAGAAATGGAGGAGAGAAATCCACAGT 1794
 QY 1681 TCCTGATAGTCTCATTTGAGCTCTCGATCCAGTCTTTCTGAAGCTGTGTTTCTCTGG 1740
 Db 1795 TCCTGATAGTCTCATTTGAGCTCTCGATCCAGTCTTTCTGAAGCTGTGTTTCTCTGG 1854
 QY 1741 ACTTTTCATGATGTGAGGCAATAAATTTGCTTCATTTCTCTTG 1782
 Db 1855 ACTTTTCATGATGTGAGGCAATAAATTTGCTTCATTTCTCTTG 1896

RESULT 3

AA004335
 ID AAD04335 standard; cDNA; 2873 BP.

XX AC AAD04335;

XX DT 04-JUL-2001 (first entry)

DE DE Human TNF receptor-associated factor binding protein, IREN-E cDNA.

XX Human; Tumour Necrosis Factor; TNF; TNF Receptor Associated Factor;
 KW TRAF2; TRAF2 binding protein; IREN; IkappaB Regulator; IREN-E;
 KW immunosuppressive; nuclear factor-kappaB; NF-kappaB; cytostatic; tumour;
 KW AIDS; acquired immune deficiency syndrome; rheumatic disease; apoptosis;
 KW autoimmune disease; septic shock; graft-vs-host reaction; inflammation;
 KW anorexia; anti-HIV; therapy; ss.

OS Homo sapiens.

XX Key Location/Qualifiers
 PH CDS 1..2355
 FT /*tag= a
 .FT /product= "Human TRAF2-binding protein isoform, IREN-E"

XX WO200116314-A1.
 PN 08-MAR-2001.
 PD 31-AUG-2000; 2000WO-IL000517.
 PF 02-SEP-1999; 99IL-00131719.
 PR (YEDA) YEDA RES & DEV CO LTD.
 XX Wallach D, Malinin N, Sinha I, Leu S;
 PI WPI: 2001-281387/29.
 XX P-PSDB; AAE00685.
 DR New DNA sequence encoding Tumor Necrosis Factor receptor associated
 PT factor (TRAF) binding proteins (IREN) for treatment or prevention of
 PT pathological conditions associated with NF-kappaB induction.
 XX Claim 1; Fig 5; 118pp; English.

XX The present cDNA sequence encodes human tumour necrosis factor (TNF)
 CC receptor-associated factor (TRAF2) binding protein isoform, IREN-E. A
 CC fragment of this IREN-E molecule is capable of binding to TRAF2 protein
 CC at position 225-501. The invention relates to human tumour necrosis
 CC factor (TNF) receptor-associated factor (TRAF2) binding protein
 CC designated as IREN (IkappaB Regulator), its isoforms IREN-10B, IREN-E and
 CC their corresponding cDNA molecules. IREN is useful for
 CC modulating/mediating the activity of transcription factor NF (Nuclear
 CC Factor)-kappaB or any other intracellular signalling activity mediated by
 CC TRAF2. IREN is useful in the prevention and treatment of a pathological
 CC condition associated with NF-kappaB induction (abnormal) e.g. AIDS
 CC (acquired immune deficiency syndrome), autoimmune diseases, tumours,
 CC rheumatic diseases, anorexia, septic shock and graft-vs-host reactions.
 CC IREN also plays an important role in the control of inflammation and
 CC other non-apoptotic effects of TNF as well as in the control of
 CC apoptosis. The invention also relates to method for screening,
 CC identifying and producing a molecule capable of modulating activities
 CC mediated by IREN. IREN antibodies are useful for the purification of new
 CC proteins from different sources, including cell extracts or transformed
 CC cell lines, in addition IREN can be used in diagnostic purposes for
 CC identifying disorders related to abnormal functioning of cellular effects
 CC mediated directly by TRAF proteins

SQ Sequence 2873 BP; 756 A; 736 C; 806 G; 575 T; 0 U; 0 Other;

Query Match 89.5%; Score 1595; DB 4; Length 2873;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGCGGATCAGAAACAATGACAAAACAAATTTCTGCTGGAGCGACTGCTGGATGCA 60
 Db 1 ATGAGCGGATCAGAAACAATGACAAAACAAATTTCTGCTGGAGCGACTGCTGGATGCA 60
 QY 61 GTGAAACAGTGCAGATCCGCTTTGAGGGGAGAAAGAGATTGCTCGGATCCGACAGC 120
 Db 61 GTGAAACAGTGCAGATCCGCTTTGAGGGGAGAAAGAGATTGCTCGGATCCGACAGC 120
 QY 121 AGGGTCACCTGTCTGTGTGCCAGTTTGAAGCCGCTCTGCAGCATGGCTTGAAGAGAGT 180
 Db 121 AGGGTCACCTGTCTGTGTGCCAGTTTGAAGCCGCTCTGCAGCATGGCTTGAAGAGAGT 180
 QY 181 CGAGGATTTGGACTCAGCGGGCAGCGATCAAGCAGGACGCGGCTTTGCCAGCAAAACC 240
 Db 181 CGAGGATTTGGACTCAGCGGGCAGCGATCAAGCAGGACGCGGCTTTGCCAGCAAAACC 240
 QY 241 GAAACAGAGCCGCTGTCTGTGGTACTACGTGAAGAGGTCTCTCAACAGCACGAGCTGCAG 300
 Db 241 GAAACAGAGCCGCTGTCTGTGGTACTACGTGAAGAGGTCTCTCAACAGCACGAGCTGCAG 300
 QY 301 CGCTTCTACTCCCTGCGCCACATCGCTCTCAGACGTGGGCGGGGTTCGCGCTGCGTCGC 360
 Db 301 CGCTTCTACTCCCTGCGCCACATCGCTCTCAGACGTGGGCGGGGTTCGCGCTGCGTCGC 360

Db 301 CGTTTCTACTCCCTGCGGCCACATCCCTCAGACGTGGGCGGGGTCGCGCTGGCTGGC 360
Qy 361 TGTGCGCTCAACGAACACTCCCTGAGCGGTACCTGCACATGCTCTCTGGCCGACCGCTGC 420
Db 361 TGTGCGCTCAACGAACACTCCCTGAGCGGTACCTGCACATGCTCTCTGGCCGACCGCTGC 420
Qy 421 AGGCTGAGCATTCTTATGAAGACTGGTCTCTTTGTGATGATGAAGAGGTCCAGTATG 480
Db 421 AGGCTGAGCATTCTTATGAAGACTGGTCTCTTTGTGATGATGAAGAGGTCCAGTATG 480
Qy 481 CTCTCTACATGGCAGCAGGTCTGAACCTCCATCTCTTTGGATTTAAACATGCACACAAG 540
Db 481 CTCTCTACATGGCAGCAGGTCTGAACCTCCATCTCTTTGGATTTAAACATGCACACAAG 540
Qy 541 GATTTGAA CGGCGAGTAAAGTTTGTCTCCACCGTTTCAGACCTCTTAAAGAGTCAACG 600
Db 541 GATTTGAA CGGCGAGTAAAGTTTGTCTCCACCGTTTCAGACCTCTTAAAGAGTCAACG 600
Qy 601 CAGAACGTGACTCTCTGCTGAAGAGTCCAGGACGAGGAGTGAAGCCTGTTTCAAGGAG 660
Db 601 CAGAACGTGACTCTCTGCTGAAGAGTCCAGGACGAGGAGTGAAGCCTGTTTCAAGGAG 660
Qy 661 ATCAGAGCTCTCTGCGCTCTCCATCTCATCAAACTGAACAGGACGACCCCTTG 720
Db 661 ATCAGAGCTCTCTGCGCTCTCCATCTCATCAAACTGAACAGGACGACCCCTTG 720
Qy 721 CCTCTGCTGCCAGGAATGTGAGTCTGATGCCAAATGCAAAAAGGAGCGGAAAGAAA 780
Db 721 CCTCTGCTGCCAGGAATGTGAGTCTGATGCCAAATGCAAAAAGGAGCGGAAAGAAA 780
Qy 781 AAGAAAGTGACCAATATCTATTGATGATGAAGAGTGAAGCAATCTTGGGGAC 840
Db 781 AAGAAAGTGACCAATATCTATTGATGATGAAGAGTGAAGCAATCTTGGGGAC 840
Qy 841 GTGTTTAAAAAGACACCTTGGGCGAGGAGCTCAGAGGCAACTCCGACCGCTCTCT 900
Db 841 GTGTTTAAAAAGACACCTTGGGCGAGGAGCTCAGAGGCAACTCCGACCGCTCTCT 900
Qy 901 GTCAATATCATGTCCGCTTTGAAAGCCCTTCCGGCTTAACCTCAATGGAAGTCAGAGC 960
Db 901 GTCAATATCATGTCCGCTTTGAAAGCCCTTCCGGCTTAACCTCAATGGAAGTCAGAGC 960
Qy 961 AGCAACTCATGGAAAAATGATTCCTGTCTTTGAACGGGGAGTTTGGGTACCAAGAGCTT 1020
Db 961 AGCAACTCATGGAAAAATGATTCCTGTCTTTGAACGGGGAGTTTGGGTACCAAGAGCTT 1020
Qy 1021 GATGTGAAAAGCATCGATGATGAAGATGTGATGAAAACGAGATGACGTGTATGGAAC 1080
Db 1021 GATGTGAAAAGCATCGATGATGAAGATGTGATGAAAACGAGATGACGTGTATGGAAC 1080
Qy 1081 TCATCAGGAAGGAAGCACAGGGGCCACTCGGAGTCGCCGAGAACCACTGGAAGGGAAAC 1140
Db 1081 TCATCAGGAAGGAAGCACAGGGGCCACTCGGAGTCGCCGAGAACCACTGGAAGGGAAAC 1140
Qy 1141 ACCTGCTCTCCAGATGCAAGCTGGGCTCCGCTGAAGGTGCTGCAAAATGACTCCGAC 1200
Db 1141 ACCTGCTCTCCAGATGCAAGCTGGGCTCCGCTGAAGGTGCTGCAAAATGACTCCGAC 1200
Qy 1201 ATCTCTTCTCCCTGTCAGTGGGCTCTACAGCCAGAGATGCCCTCCGAGC 1260
Db 1201 ATCTCTTCTCCCTGTCAGTGGGCTCTACAGCCAGAGATGCCCTCCGAGC 1260
Qy 1261 CTGGAGAACGGGACAGGACCAAGAGACCACTTCTCCGGATCTCTGGAAGTTCGGTACAGT 1320
Db 1261 CTGGAGAACGGGACAGGACCAAGAGACCACTTCTCCGGATCTCTGGAAGTTCGGTACAGT 1320
Qy 1321 GTGGAAGCCAGCTCTCCAGGCCAGGAAGTCTCTGAGCAGCCTGTACCTTCTGCTCTCA 1380
Db 1321 GTGGAAGCCAGCTCTCCAGGCCAGGAAGTCTCTGAGCAGCCTGTACCTTCTGCTCTCA 1380
Qy 1381 GTGCCAGAGTCCATGACAAATAGTGAACCTGCGCCAGGACCTGTGGCCATGATGAACAGG 1440
Db 1381 GTGCCAGAGTCCATGACAAATAGTGAACCTGCGCCAGGACCTGTGGCCATGATGAACAGG 1440

Qy 1441 AAGGATGAGCTGGAGGAGGAACAGATCACTGCGAAACCTGCTCGACGGTGAGATGGAG 1500
Db 1441 AAGGATGAGCTGGAGGAGGAACAGATCACTGCGAAACCTGCTCGACGGTGAGATGGAG 1500
Qy 1501 CACTCAGCGCGCTCCGGCAAGAGGTGGACACCTTTGAAAAGGAGGTGGCTGAAACAGAG 1560
Db 1501 CACTCAGCGCGCTCCGGCAAGAGGTGGACACCTTTGAAAAGGAGGTGGCTGAAACAGAG 1560
Qy 1561 GAGCGGAGGCGATGAAGGTCCAGGCGCTGGCCAG 1595
Db 1561 GAGCGGAGGCGATGAAGGTCCAGGCGCTGGCCAG 1595

RESULT 4
AAD04334
ID AAD04334 standard; cDNA; 3139 BP.
XX
AC AAD04334;
XX
DT 04-JUL-2001 (first entry)
XX
DE Human TNF receptor-associated factor binding protein, IREN-10B cDNA.
XX
KW Human; Tumour Necrosis Factor; TNF; TNF Receptor Associated Factor;
TRAF2; TRAF2 binding protein; IkappaB Regulator; IREN-10B;
immunosuppressive; nuclear factor-kappaB; NF-kappaB; cytostatic; tumour;
AIDS; acquired immune deficiency syndrome; rheumatic disease; apoptosis;
autoimmune disease; septic shock; graft-vs-host reaction; inflammation;
anorexia; anti-HIV; therapy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..2442
FT /*tag= a
FT /product= "Human TRAF2-binding protein isoform, IREN-10B"
XX
PN WO200116314-A1.
XX
PD 08-MAR-2001.
XX
PF 31-AUG-2000; 2000WO-IL000517.
XX
PR 02-SEP-1999; 99IL-00131719.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Wallach D, Malinin N, Sinha I, Leu S;
XX
WPI; 2001-281387/29.
P-PSDB; AAE00684.
XX
PT New DNA sequence encoding Tumor Necrosis Factor receptor associated
factor (TRAF) binding proteins (IREN) for treatment or prevention of
pathological conditions associated with NF-kappaB induction.
XX
PS Claim 1; Fig 4; 118pp; English.
XX
CC The present cDNA sequence encodes human tumour necrosis factor (TNF)
receptor-associated factor (TRAF2) binding protein isoform, IREN-10B. A
fragment of this IREN-10B molecule is capable of binding to TRAF2 protein
at position 225-501. The invention relates to human tumour necrosis
factor (TNF) receptor- associated factor (TRAF2) binding protein
designated as IREN (IkappaB Regulator). IREN is useful for
modulating/mediating the activity of transcription factor NF (Nuclear
Factor)-kappaB or any other intracellular signalling activity mediated by
TRAF2. IREN is useful in the prevention and treatment of a pathological
condition associated with NF-kappaB induction (abnormal) e.g. AIDS
(acquired immune deficiency syndrome), autoimmune diseases, tumours,
rheumatic diseases, anorexia, septic shock and graft-vs-host reactions.
CC IREN also plays an important role in the control of inflammation and

CC other non-apoptotic effects of TNF as well as in the control of
CC apoptosis. The invention also relates to method for screening,
CC identifying and producing a molecule capable of modulating activities
CC mediated by IREN. IREN antibodies are useful for the purification of new
CC proteins from different sources, including cell extracts or transformed
CC cell lines, in addition IREN can be used in diagnostic purposes for
CC identifying disorders related to abnormal functioning of cellular effects
CC mediated directly by TRAF proteins
XX
SQ Sequence 3139 BP; 797 A; 851 C; 875 G; 616 T; 0 U; 0 Other;
Query Match 89.5%; Score 1595; DB 4; Length 3139;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGCGGATCACAGAACATGACAAAGACAAATTTCTGCTGGAGGACTGCTGGATGCA 60
DB 1 ATGAGCGGATCACAGAACATGACAAAGACAAATTTCTGCTGGAGGACTGCTGGATGCA 60
QY 61 GTGAACAGTCCAGATCCGCTTTGGAGGGAGAAAGAGATTCCCTCGGATTCGGACAGC 120
DB 61 GTGAACAGTCCAGATCCGCTTTGGAGGGAGAAAGAGATTCCCTCGGATTCGGACAGC 120
QY 121 AGGGTCACCTGTCTGTGTCGCCAGTTTGAAGCCGCTCTGCAGCATGCTTTGAAGAGGAGT 180
DB 121 AGGGTCACCTGTCTGTGTCGCCAGTTTGAAGCCGCTCTGCAGCATGCTTTGAAGAGGAGT 180
QY 181 CGAGGATTTGGCACTCACAGCGGAGCGGATCAAGCAGGAGCGGGCTTTGCGACAAACC 240
DB 181 CGAGGATTTGGCACTCACAGCGGAGCGGATCAAGCAGGAGCGGGCTTTGCGACAAACC 240
QY 241 GAAACAGAGCCGTGTTCTGGTACTAGTGAAGAGGAGTCTCAACAGACAGAGCTGCAG 300
DB 241 GAAACAGAGCCGTGTTCTGGTACTAGTGAAGAGGAGTCTCAACAGACAGAGCTGCAG 300
QY 301 CGCTTCTACTCTCGGCCACATCGCTCAGAGTGGCGGGGTCGCGCTCGCTCGCG 360
DB 301 CGCTTCTACTCTCGGCCACATCGCTCAGAGTGGCGGGGTCGCGCTCGCTCGCG 360
QY 361 TGTGCCCTCAACGAACACTCCCTGGAGCGCTACCTGCACATGCTCTGCGCCGCGCTGC 420
DB 361 TGTGCCCTCAACGAACACTCCCTGGAGCGCTACCTGCACATGCTCTGCGCCGCGCTGC 420
QY 421 AGGCTGAGCACTTTTATGAAGACTGGTCTTTTGTGATGGATGAAGAAAGGTCCAGTATG 480
DB 421 AGGCTGAGCACTTTTATGAAGACTGGTCTTTTGTGATGGATGAAGAAAGGTCCAGTATG 480
QY 481 CTTCTTACCATGGCAGAGGTCTGAATCCATCTCTTTCCGATTAACATCGACAACAG 540
DB 481 CTTCTTACCATGGCAGAGGTCTGAATCCATCTCTTTCCGATTAACATCGACAACAG 540
QY 541 GATTGAAACGGGAGAGTAAAGTTGTCTCCACCGTTTCAGACCTCTTAAAGAGTCAACG 600
DB 541 GATTGAAACGGGAGAGTAAAGTTGTCTCCACCGTTTCAGACCTCTTAAAGAGTCAACG 600
QY 601 CAGAACGTGACCTCTTCTGAGGAGTCCACCGAGAGTGCAGCCTGTTTCAGGGAG 660
DB 601 CAGAACGTGACCTCTTCTGAGGAGTCCACCGAGAGTGCAGCCTGTTTCAGGGAG 660
QY 661 ATCAGAGCCTCTCTGCGCTCTCCATCCTCATCAAACTTGAACAGGAGACCGCCCTTG 720
DB 661 ATCAGAGCCTCTCTGCGCTCTCCATCCTCATCAAACTTGAACAGGAGACCGCCCTTG 720
QY 721 CTTGTGTGTCCAGGAATGTCAGTGTCTGATGCGCAATGCAAAAGGAGCGGAGAGAAA 780
DB 721 CTTGTGTGTCCAGGAATGTCAGTGTCTGATGCGCAATGCAAAAGGAGCGGAGAGAAA 780
QY 781 AAGAAAGTGAACCAATCTCAATTTGATGAGGAGAGTGAAGAGTCTTGGGGAC 840
DB 781 AAGAAAGTGAACCAATCTCAATTTGATGAGGAGAGTGAAGAGTCTTGGGGAC 840
QY 841 GTGTTTTAAAGACACCTGGGCGGAGGAGGCTCAGAGGACAACTCCGACCGCTCTCT 900
DB 841 GTGTTTTAAAGACACCTGGGCGGAGGAGGCTCAGAGGACAACTCCGACCGCTCTCT

DB 841 GTGTTTTAAAGACACCTGGGCGGAGGAGGCTCAGAGGACAACTCCGACCGCTCTCT 900
QY 901 GTCAATATCATGTCCGCTTTTGAAGCCCTTTCGGGCTTAATCCAATGGAAGTCAGAGC 960
DB 901 GTCAATATCATGTCCGCTTTTGAAGCCCTTTCGGGCTTAATCCAATGGAAGTCAGAGC 960
QY 961 AGCAACTCATGAAATATGATTCCTGCTTTTGAACGGGAGTTTGGGTACCAAGACCTT 1020
DB 961 AGCAACTCATGAAATATGATTCCTGCTTTTGAACGGGAGTTTGGGTACCAAGACCTT 1020
QY 1021 GATGTGAAAGCATCGATGATGAGATGAAAGCAAGATGACGCTGTATGGAAC 1080
DB 1021 GATGTGAAAGCATCGATGATGAGATGAAAGCAAGATGACGCTGTATGGAAC 1080
QY 1081 TCATCAGGAAGGAAGCAGAGGGCCACTCGAGTCCGCCGAGAACCACTGGAAGGGAAC 1140
DB 1081 TCATCAGGAAGGAAGCAGAGGGCCACTCGAGTCCGCCGAGAACCACTGGAAGGGAAC 1140
QY 1141 ACCTGCTCTCCAGATGCACAGCTGGCTCCGCTGAAGGTGCTGCACATGACTCCGAC 1200
DB 1141 ACCTGCTCTCCAGATGCACAGCTGGCTCCGCTGAAGGTGCTGCACATGACTCCGAC 1200
QY 1201 ATCTCTTCTCCAGTGGCTCTTACAGCCAGCAGATGCCCCCTCGGAAGC 1260
DB 1201 ATCTCTTCTCCAGTGGCTCTTACAGCCAGCAGATGCCCCCTCGGAAGC 1260
QY 1261 CTGGAGAACGGGACAGGACACAGTCTCCCGGATCTCGGACTTCGGTACAGT 1320
DB 1261 CTGGAGAACGGGACAGGACACAGTCTCCCGGATCTCGGACTTCGGTACAGT 1320
QY 1321 GTGGAGAACGGGACACAGTCTCCAGGACCAAGTCTCTGAGCAGCTGTACCTTCTGCTCA 1380
DB 1321 GTGGAGAACGGGACACAGTCTCCAGGACCAAGTCTCTGAGCAGCTGTACCTTCTGCTCA 1380
QY 1381 GTGCCAGAGTCCATGACAAATAGTGAATAGTGAATAGTGAATAGTGAATAGTGAATAGT 1440
DB 1381 GTGCCAGAGTCCATGACAAATAGTGAATAGTGAATAGTGAATAGTGAATAGTGAATAGT 1440
QY 1441 AAGGATGAGTGGAGAGGAGAACAGATCACTGCGAAACCTGCTCGACCGTGAAGTGAG 1500
DB 1441 AAGGATGAGTGGAGAGGAGAACAGATCACTGCGAAACCTGCTCGACCGTGAAGTGAG 1500
QY 1501 CACTCAGCGCGCTCCGGAAGAGGTGAGACCTCTGAAAGAGGTGCTGAAACAGGAG 1560
DB 1501 CACTCAGCGCGCTCCGGAAGAGGTGAGACCTCTGAAAGAGGTGCTGAAACAGGAG 1560
QY 1561 GAGCGCAGGCGCATGAAGTCCAGGCGCTGGCCAG 1595
DB 1561 GAGCGCAGGCGCATGAAGTCCAGGCGCTGGCCAG 1595

RESULT 5
AAH15665
ID AAH15665 standard; cDNA; 2248 BP.
XX
AC AAH15665;
XX AC
XX AC
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA sequence SRQ ID NO:14016.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX Homo sapiens.
XX
XX EP1074617-A2.
XX
XX 07-FEB-2001.
PD
XX 28-JUL-2000; 2000EP-00116126.
PF
XX 29-JUL-1999; 99JP-00248036.
PR 27-AUG-1999; 99JP-00300253.
PR

PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX (HELI-) HELIX RES INST.
XX
XX
PI Ota T, Isegai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX WPI; 2001-318749/34.
XX
XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT length cDNAs defined in the specification, and for the detection and/or
PT diagnosis of the abnormality of the proteins encoded by the full-length
PT cDNAs.
XX
XX Claim 8; SEQ ID NO 14016; 2537pp + Sequence Listing; English.
XX
XX The present invention describes primer sets for synthesizing 5602 full-
CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to AAH95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention
XX
XX Sequence 2248 BP; 548 A; 548 C; 618 G; 534 T; 0 U; 0 Other;

Query Match 63.4%; Score 1129.8; DB 4; Length 2248;
Best Local Similarity 95.3%; Pred. No. 1.1e-297;
Matches 1164; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

Qy 1 ATGAGCGGATCACAGAACAAATGACAAAGACAAATTTCTGCTGGAGCGACTCTGGATGCA 60
Db 63 ATGAGCGGATCACAGAACAAATGACAAAGACAAATTTCTGCTGGAGCGACTCTGGATGCA 122
Qy 61 GTGAAACAGTCCAGATCCGCTTTGGAGGAGAAAGAGATTTGCTCGGATTCGACACAGC 120
Db 123 GTGAAACAGTCCAGATCCGCTTTGGAGGAGAAAGAGATTTGCTCGGATTCGACACAGC 182
Qy 121 AGGCTACCTGTCTGTGTGCCAGTTTGAAGCCGCTCTGACAGATGGCTTGAAGAGGAGT 180
Db 183 AGGCTACCTGTCTGTGTGCCAGTTTGAAGCCGCTCTGACAGATGGCTTGAAGAGGAGT 242
Qy 181 CGAGGATGGGCACTCACAGCGGCGGCGATCAAGCAGGCGGGCTTTGCCAGCAAAACC 240
Db 243 CGAGGATGGGCACTCACAGCGGCGGCGATCAAGCAGGCGGGCTTTGCCAGCAAAACC 302
Qy 241 GAAACAGAGCCGCTGTCTGTGTACTACGTGAAGAGGTCCTCAACAGCAGAGCTGCAG 300
Db 303 GAAACAGAGCCGCTGTCTGTGTACTACGTGAAGAGGTCCTCAACAGCAGAGCTGCAG 362
Qy 301 CGCTTTACTCCCTCGCCACATCGCCTCAGACGTGGCCGGGGTCGCGCTTGGCTGCGC 360
Db 363 CGCTTTACTCCCTCGCCACATCGCCTCAGACGTGGCCGGGGTCGCGCTTGGCTGCGC 422
Qy 361 TGTGCGCTCAAGCAACTCCCTGGAGCGCTACCTGCACATGCTCTCTGGCCGCGGCTGC 420

Db 423 TGTGCCCTCAACGAACACTCCCTGGAGCGCTACCTGCACATGCTCTCTGGCCGACCGCTGC 482
Qy 421 AGGCTGAGCACTTTTATGAAGACTGGTCTTTTGTGATGGATGAAGAAGGTTCCAGTATG 480
Db 483 AGGCTGAGCACTTTTATGAAGACTGGTCTTTTGTGATGGATGAAGAAGGTTCCAGTATG 542
Qy 481 CTTCTTACCATTGGCAGCAGGTCTGAATCTCCATCTTTTGGCATTTAAATCGACAAACAG 540
Db 543 CTTCTTACCATTGGCAGCAGGTCTGAATCTCCATCTTTTGGCATTTAAATCGACAAACAG 602
Qy 541 GATTGACAGCGGCGAGAGTAAAGTTTGTCTCCACCGCTTTTCAGACCTCTTAAAGGAGTCAACG 600
Db 603 GATTGACAGCGGCGAGAGTAAAGTTTGTCTCCACCGCTTTTCAGACCTCTTAAAGGAGTCAACG 662
Qy 601 CAGAACGTGACCTCTCTTGTCTGAAGAGTCCACGCAAGGAGTGAGCAGCCTGTTCAGGGAG 660
Db 663 CAGAACGTGACCTCTCTTGTCTGAAGAGTCCACGCAAGGAGTGAGCAGCCTGTTCAGGGAG 722
Qy 661 ATCAAGCCTCTCTGCGCTCTCCATCTCATATCAAACTGAAACGAGGAGACCGACCCCTTG 720
Db 723 ATCAAGCCTCTCTGCGCTCTCCATCTCATCAAACTGAAACGAGGAGACCGACCCCTTG 782
Qy 721 CCTCTCTGTCAGGAATGTCTAGTCTGATGCCAAATGCCAAAGAGGCGGAAGAGAAA 780
Db 783 CCTCTCTGTCAGGAATGTCTAGTCTGATGCCAAATGCCAAAGAGGCGGAAGAGAAAG 842
Qy 781 AAGAAAGTGACCAACAATAATCTCATTTGATGAGGAGAGATGAGCAAACTCTGGGGAC 840
Db 843 AAGAAAGTGACCAACAATAATCTCATTTGATGAGGAGAGATGAGCAAACTCTGGGGAC 902
Qy 841 GTGTTTAAAAAGACACCTGGGGCAGGGGAGAGCTCAGAGGACAACTCCGACCGCTCTCT 900
Db 903 GTGTTTAAAAAGACACCTGGGGCAGGGGAGAGCTCAGAGGACAACTCCGACCGCTCTCT 962
Qy 901 GTCAATATCATGTCCGCTTTGAAGCCCTTTGGAGCCCTTAATCTCAATGGAAGTCAAGC 960
Db 963 GTCAATATCATGTCCGCTTTGAAGCCCTTTGGAGCCCTTAATCTCAATGGAAGTCAAGC 1022
Qy 961 AGCAACTCATGGAATAATGATTCCCTGTCTTGAACGGGGAGTTTGGGTACCAAGCTT 1020
Db 1023 AGCAACTCATGGAATAATGATTCCCTGTCTTGAACGGGGAGTTTGGGTACCAAGCTT 1082
Qy 1021 GATGTGAAAGCATCGATGATGAAGATGTGATGAAACCGAAGATGACGTGTATGGAAC 1080
Db 1083 GATGTGAAAGCATCGATGATGAAGATGTGATGAAACCGAAGATGACGTGTATGGAAC 1142
Qy 1081 TCATCAGGAAGGAGCAGCGGCGCACTCGAGTTCGCCCGAGAGCCACTTGAAGGGGAAAC 1140
Db 1143 TCATCAGGAAGGAGCAGCGGCGCACTCGAGTTCGCCCGAGAGAGTAAAGTTTGTGTGTA 1202
Qy 1141 ACCTGCTCTCCAGATGACAGCTGGGCTCCGCTGAAGGTGCTGCACAAATGACTCCGAC 1200
Db 1203 GGTGAGTCTCACCGTCCCGCAGGCTGGAGTCCGCTGGCTGATCTCAGTCTCACTGCAAC 1262
Qy 1201 ATCTCTTTCCTGTCACTGGC 1221
Db 1263 CTCCACCTCCCGGTTTCAGGC 1283

RESULT 6
AAH18235
ID AAH18235 standard; cDNA; 6045 BP.
XX
XX AAH18235;
XX
XX 26-JUN-2001 (first entry)
XX
XX Human cDNA sequence SEQ ID NO:18174.
DE Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
XX Homo sapiens.
XX

PN EP1074617-A2.
XX 07-FEB-2001.
XX 28-JUL-2000; 2000EP-00116126.
XX 29-JUL-1999; 99JP-00248036.
PR 27-AUG-1999; 99JP-00300253.
PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX (HELI-) HELIX RES INST.
XX Ota T, Isogai T, Nishikawa T, Hayaishi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNA.
PT
PT
XX
PS Claim 8; SEQ ID NO 18174; 2537pp + Sequence Listing; English.
XX
CC The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 3'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesizing polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention
XX
SQ Sequence 6045 BP; 1561 A; 1493 C; 1427 G; 1564 T; 0 U; 0 Other;

Query Match 45.8%; Score 816.8; DB 4; Length 6045;
Best Local Similarity 97.0%; Pred. No. 6e-212;
Matches 854; Conservative 0; Mismatches 22; Indels 4; Gaps 2;
QY 246 AGAGCCCGTGTCTTGGTACTACGTGAAGGAGCTCTCAACAGCAGAGCTGC-AGCGCT 304
DB 932 AAAGCCCGTGTCTTGGTACTACGTGAAGGAGCTCTCAACAGCAGAGCTGC-AGCGCT 991
QY 305 TCTACTCCCTCGCGCACATCGCTCAGACGTGGGCGCGGCTCGCGCTGGCTGTG 364
DB 992 TCTACTCCCTCGCGCACATCGCTCAGACGTGGGCGCGGCTCGCGCTGGCTGTG 1051
QY 365 CCTCAACGAACACTCCCTGGAGCGCTACTGACATGCTCTGGCGCAGCGCTGACGC 424
DB 1052 CCTCAACGAACACTCCCTGGAGCGCTACTGACATGCTCTGGCGCAGCGCTGACGC 1111
QY 425 TGAGCACTTTTATGAACATGCTCTTGTGATGATGAAGAGTCCAGTATGCTTC 484
DB 1112 TCAGTACTTTTATGAAGATGGTCTTTGTGATGATGAAGAGTCCAGTATGCTTC 1171
QY 485 CTACCATGGCAGCAGGTCTCTGAACCTCCACTCTTTGGATTAAACATCACAACAGGATT 544

DB 1172 CTACCATGGCAGCAGGTCCGAACTCCATACTCTTTGGATTAACTTGAACAAGGATT 1231
QY 545 TGAACGGGCGAGAGTAAGTTTGTCTCCACCGTTTTCAGACCTCTTTAAAGGAGTCAACGCAGA 604
DB 1232 TGAACGGGCGAGAGTAAGTTTGTCTCCACCGTTTTCAGACCTCTTTAAAGGAGTCAACGCAGA 1291
QY 605 AGCTGACCTCCCTTGTCTGAAGGAGTCCACGCAAGGAGTGAAGAGTCTTTCAGGGAGATCA 664
DB 1292 ATGTGA---CCCTGTCTGAAGGAGTCCACGCAAGGAGTGAAGAGTCTTTCAGGGAGATCA 1348
QY 665 CAGCCTCTCTCTGCGGTCTCCATCTCTCATCAAACTGAAACAGGAGACCGACCCCTTGCCTG 724
DB 1349 CAGCCTCTCTCTGCGGTCTCCATCTCTCATCAAACTGAAACAGGAGACCGACCCCTTGCCTG 1408
QY 725 TCGTGTCCAGGAATGTCTAGTGTCTGATGCGCAATGCAAAAAGGAGCGGAAGAGAAAAGA 784
DB 1409 TCGTGTCCAGGAATGTCTAGTGTCTGATGCGCAATGCAAAAAGGAGCGGAAGAGAAAAGC 1468
QY 785 AAGTGACCAACAATAATCTCATTTTGATGATGAGGAGATGAGCAGAACTCTGGGACGTGT 844
DB 1469 AAGTGACCAACAATAATCTCATTTTGATGATGAGGAGATGAGCAGAACTCTGGGACATGT 1528
QY 845 TTAATAAGACACTCGGGCAGGGAGAGCTCAGAGACAACTCCGACCCCTCTCTGTCTCA 904
DB 1529 TTAATAAGACACTCGGGCAGGGAGAGCTCAGAGACAACTCCGACCCCTCTCTGTCTCA 1588
QY 905 ATATCATGTCCGCTTTGAAAGCCCTTCGGGCTTAACTCCAATGGAAGTCAGAGCAGCA 964
DB 1589 ATATCATGTCCGCTTTGAAAGCCCTTCGGGCTTAACTCCAATGGAAGTCAGAGCAGCA 1648
QY 965 ACTCATGGAAAAATTGATTCCTCTGTTTCAACGGGAGTTTGGGTACCAAGAGCTTGATG 1024
DB 1649 ACTCTGGAAAAATTGATTCCTCTGTTTCAACGGGAGTTTGGGTACCAAGAGCTTGATG 1708
QY 1025 TGAAGAAGCATCATGATGAAGATGTGGATGAAAAAGAGATCACTGTATGGAACACTCAT 1084
DB 1709 TGAAGAAGCATCATGATGAAGATGTGGATGAAAAAGAGATCACTGTATGGAACACTCAT 1768
QY 1085 CAGGAAGGAGACACAGGGCCACTCGGAGTCCGCCGAGAA 1124
DB 1769 CAGGAAGGAGACACAGGGCCACTCGGAGTCCGCCGAGAA 1808
RESULT 7
AAH04973
ID AAH04973 standard; cDNA; 730 BP.
XX
AC AAH04973;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA clone (5'-primer) SEQ ID NO:1808.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; BR.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-00116126.
XX
PR 29-JUL-1999; 99JP-00248036.
PR 27-AUG-1999; 99JP-00300253.
PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayaishi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX WPI; 2001-318749/34.

XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

XX Claim 1; SEQ ID NO 1808; 2537pp + Sequence Listing; English.

XX The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesizing polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention

XX SQ Sequence 730 BP; 173 A; 200 C; 217 G; 137 T; 0 U; 3 Other;

Query Match 35.9%; Score 639.8; DB 4; Length 730;
Best Local Similarity 99.0%; Pred. No. 5e-164;
Matches 663; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

QY 1 ATGAGCGGATCACAGAAACAATGACAAAAGACAATTTCTGCTGGAGCGCACTGCTGGATGCA 60
DB 63 ATGAGCGGATCACAGAAACAATGACAAAAGACAATTTCTGCTGGAGCGCACTGCTGGATGCA 122

QY 61 GTCAAAACAGTCCAGATCCGCTTTGGAGGGAGAAAGAGATGCTCGGATTCGACAGC 120
DB 123 GTGAAACAGTCCAGATCCGCTTTGGAGGGAGAAAGAGATGCTCGGATTCGACAGC 182

QY 121 AGGTCACCTGTCTGTGTGCCAGTTTGAAGCCCTCTGACGATGCGCTTGAAGAGAGT 180
DB 183 AGGTCACCTGTCTGTGTGCCAGTTTGAAGCCCTCTGACGATGCGCTTGAAGAGAGT 242

QY 181 CGAGGATTGGCACTCAGAGCGGCGCATCAAGCAGCAGCGGGCTTTGCCAGCAAAACC 240
DB 243 CGAGGATTGGCACTCAGAGCGGCGCATCAAGCAGCAGCGGGCTTTGCCAGCAAAACC 302

QY 241 GAAACAGAGCCGCTGTTCTGTACTACGTGAAGAGGTCTCTCAACAGCAGAGCTCGAG 300
DB 303 GAAACAGAGCCGCTGTTCTGTACTACGTGAAGAGGTCTCTCAACAGCAGAGCTCGAG 362

QY 301 CGCTTCTACTCCCTGCGCCACATCCCTCAGACGTGGCGGGGTGCGGCTGCGCTGCGC 360
DB 363 CGCTTCTACTCCCTGCGCCACATCCCTCAGACGTGGCGGGGTGCGGCTGCGCTGCGC 422

QY 361 TGTGCGCTCAACGAACACTCCCTGGAGCGCTTACCTGCACATGCTCTCTGGCGGCGCGTGC 420
DB 423 TGTGCGCTCAACGAACACTCCCTGGAGCGCTTACCTGCACATGCTCTCTGGCGGCGCGTGC 482

QY 421 AGCTGAGCACTTTTATGAAGACTGGTCTTTTGTGATGATGAAGAAAGTCCAGTATG 480
DB 483 AGCTGAGCACTTTTATGAAGACTGGTCTTTTGTGATGATGAAGAAAGTCCAGTATG 542

QY 481 CTTCTCTACCATGGCAGAGGTCTGAACCTCCATCTCTTTGGGATTAAATCGACAAACAG 540

DB 543 CTTCTACCATGGCAGAGGTCTGAACCTCCATCTCTTTGGGATTAAATCGACAAACAG 602

QY 541 GATTGGAACGGGAGAGTAAGTTTGTCTCCACCGTTTTCAGACCTCTTAAAGGAGTCAACG 600
DB 603 GATTGGAACGGGAGAGTAAGTTTGTCTCCACCGTTTTCAGACCTCTTAAAGGAGTCAACG 662

QY 601 CAGAACCTGACCTCTCTTGTCTGAAGAGTCCACGCAAGAGTGGAGCAGCCTGTTTCAGGGAG 660
DB 663 CANAACGTGA-CTNCTTGTCTGAAGAGTCCACGCAAGAGTGGANCA-CTTGTTCAGAGGAG 720

QY 661 ATCACAGCCT 670
DB 721 ATCACAGCCT 730

RESULT 8
NAK67282
ID AAK67282 standard; DNA; 33147 BP.
XX AAK67282;
AC AAK67282;
XX
DT 06-NOV-2001 (first entry)
XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22094.
DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cytostatic; gene therapy; vaccine; metastasis; ds.
KW
XX Homo sapiens.
OS
XX WO200157182-A2.
FN
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001354.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 14-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
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PR 14-AUG-2000; 2000US-0224519P.
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PR 14-AUG-2000; 2000US-0225757P.
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PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226688P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.

QY 926 GCCCTTGGCCCTAATCTCAATGAAAGTCAGACGAGCAACTCATGGAATTTGATCCCC 985
D 9074 GCCCTTGGCCCAAACTCCAATGGAAGTCAGACGAGCAACTCTGGAAATTTGATCCCC 9133
QY 986 TGTCTTTGACCGGGAGTTGGGTACCAAGCTTGATGTAAGCAATCATCATGAAG 1045
D 9134 TGTCTTTGACCGGGAGTTGGGTACCAAGCTTGATGTAAGCAATCATCATGAAG 9193
QY 1046 ATGTGGATGAAAACCAAGATGACCTGTGTATGAAACTCATCAGGAAGCAACAGGGGCC 1105
D 9194 ATGTGGATGAAAACCAAGATGACCTGTGTATGAAACTCATCAGGAAGCAACAGGGGCC 9253
QY 1106 ACTCGAGTCCCGAGAGCACT 1130
D 9254 ACTCAGAGTCGCCCGAGAGTAAGT 9278
RESULT 9
ABS72233
ID ABS72233 standard; cDNA; 280 BP.
XX
AC ABS72233;
XX
DT 03-DEC-2002 (first entry)
XX
XX Human gene trapped sequence (GTS) #193.
XX Human; gene trapped sequence; GTS; gene; ss; cancer; autoimmune disease;
KW lupus; scleroderma; Crohn's disease; multiple sclerosis; immune disorder;
KW inflammatory bowel disease; schizophrenia; psychosis; osteoarthritis;
KW rheumatoid arthritis; diabetes; skin disorder; acne; eczema; asthma;
KW cardiovascular disease; hypertension; atherosclerosis; Alzheimer's disease;
KW viral infection; parasitic infection; fungal infection;
KW bacterial infection; forensic analysis; cellular differentiation.
XX
XX Homo sapiens.
OS
XX US2002095031-A1.
XX
XX 18-JUL-2002.
XX
XX 03-MAY-2000; 2000US-00563817.
XX
XX 04-MAY-1999; 99US-0132343P.
XX
XX (NEHL/) NEHLS M C.
PA (ZAMB/) ZAMBROWICZ B.
PA (SAND/) SANDS A T.
XX
XX Nehls MC, Zambrowicz B, Sands AT;
PI
XX WPI; 2002-656030/70.
XX
XX New isolated or purified human gene trapped sequences, useful for gene
PT discovery, as markers for gene expression analysis, identifying and
PT mapping the coding regions of human genome, or determining the genetic
PT basis of human disease.
XX
XX Claim 1; SEQ ID NO 201; 36pp; English.
PS
XX The invention relates to isolated or purified polynucleotides that
CC correspond to human gene trapped sequences (GTSs). The human GTSs are
CC useful for gene discovery and as markers for gene expression analysis,
CC for identifying and mapping the coding regions of the mammalian,
CC particularly human, genome, for forensic analysis, and for determining
CC the genetic basis of human disease. The peptides and proteins encoded by
CC the polynucleotides are useful for generating antibodies, as reagents in
CC diagnostic assays and in identifying other cellular gene products
CC involved in the regulation of development and cellular differentiation of
CC various cell types. The peptides are also useful as reagents in assays
CC for screening of compounds used in treating disorders affecting

CC development and cell differentiation. The GTSs are also useful in
CC treating or ameliorating diseases associated with the expression of
CC mutant or normal variants of the GTSs, e.g. cancer, autoimmune diseases,
CC lupus, scleroderma, Crohn's disease, multiple sclerosis, inflammatory
CC bowel disease, immune disorders, schizophrenia, psychosis, inflammatory
CC disorders, diabetes, skin disorders such as acne or eczema,
CC osteoarthritis, rheumatoid arthritis, hypertension, atherosclerosis,
CC cardiovascular diseases, Alzheimer's disease, Parkinson's disease,
CC osteoporosis, asthma, infertility, and viral, parasitic, fungal or
CC bacterial infections. This sequence represents a human GTS of the
CC invention
XX
SQ Sequence 280 BP; 71 A; 66 C; 91 G; 51 T; 0 U; 1 Other;
Query Match 15.5%; Score 275.8; DB 6; Length 280;
Best Local Similarity 98.9%; Pred. No. 9.2e-65;
Matches 277; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1349 GTCTCTGAGCAGCCTTTACCTTTCCTTCAGTGCAGAGTCCATGACAAATTAGTGAAC 1408
D 1 GGCTATGAGCAGCCTGNTACCTTTCCTTCAGTGCAGAGTCCATGACAAATTAGTGAAC 60
QY 1409 TGGCCAGGCCACTGTGCGCCATGATGAACAGGAAGGATGAGTGGAGGAGAGACAGAT 1458
D 61 TGGCCAGGCCACTGTGCGCCATGATGAACAGGAAGGATGAGTGGAGGAGAGACAGAT 120
QY 1469 CACTGCGAAAACCTGCTCGACGGTGAGATGAGCACTCAGCGCGCTCCGGCAAGAGGTGG 1528
D 121 CACTGCGAAAACCTGCTCGACGGTGAGATGAGCACTCAGCGCGCTCCGGCAAGAGGTGG 180
QY 1529 ACACCTTTGAAAAGAGAGGTGGCTGAAACAGGAGGAGCGGAGGATGAAGTCCAGGGCG 1588
D 181 ACACCTTTGAAAAGAGAGGTGGCTGAAACAGGAGGAGCGGAGGATGAAGTCCAGGGCG 240
QY 1589 TGGCCAGCTATCTTTCCTATTTTGTGAGGAGATTTCAACC 1628
D 241 TGGCCAGCTATCTTTCCTATTTTGTGAGGAGATTTCAACC 280
RESULT 10
AAS64410
ID AAS64410 standard; cDNA; 454 BP.
XX
XX AAS64410;
XX
XX AC
XX
XX 13-FEB-2002 (first entry)
XX
XX DNA encoding novel human diagnostic protein #214.
DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
XX Homo sapiens.
OS
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US008631.
XX
XX 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
PA
XX Drmanac RT, Liu C, Tang YT;
PI
XX WPI; 2001-639362/73.
DR P-PSDB; ABG00223.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess

Db 318 CCATCTCATCTCATCAAACTGAACAGGAGACCGCCCTTCCCGTGTGTCAGGA 259
QY 737 ATGTCAGTGTGATG 751
Db 258 ATGTCAGTGTGATG 244
RESULT 12
ACH89047/C
ID ACH89047 standard; DNA; 284 BP.
XX
AC ACH89047;
DT 29-JUL-2004 (first entry)
XX Human genome derived single exon probe #22242.
XX Human; probe; ss; gene expression; single exon probe; microarray;
KW alternative splicing event; genomic alteration.
XX Homo sapiens.
XX US2003194704-A1.
XX 16-OCT-2003.
XX 03-APR-2002; 2002US-00029386.
XX 03-APR-2002; 2002US-00029386.
XX (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANSZ/) HANSZEL D K.
XX Penn SG, Rank DR, Hanzel DK;
XX WPI; 2004-119264/12.
XX New human genome-derived single exon nucleic acid probes useful for human
PT gene expression analysis, for identifying or characterizing alternative
PT splicing events, for assessing genomic alterations or as tools for
PT surveying tissues.
XX Claim 1; SEQ ID NO 22242; 80pp; English.
XX The invention relates to a nucleic acid probe for measuring human gene
CC expression, comprising any of the 27,400 fully defined nucleotide
CC sequences in the specification, or their complements or fragments, and
CC encoding at least 8 amino acids of any of the 688 amino acid sequences
CC fully defined in the specification. The probe is a single exon probe that
CC hybridizes under high stringency conditions to a nucleic acid molecule
CC expressed in human cells or tissues. Also included are a spatially-
CC addressable set of single exon nucleic acid probes for measuring human
CC gene expression (comprising a plurality of single exon nucleic acid
CC probes cited above, where each of the plurality of probes is separately
CC and addressably isolatable or amplifiable from the plurality), a single
CC exon microarray for measuring human gene expression, a method of
CC measuring human gene expression, a vector comprising the single exon
CC probe cited above, an ORF-encoded peptide comprising at least 8
CC contiguous amino acids of any of the above-mentioned amino acid
CC sequences (optionally with conservative amino acid substitutions), an
CC isolated antibody that binds specifically to a peptide cited above,
CC methods of selling and/or licensing single exon probes or microarrays to
CC a customer desiring to measure gene expression, a method of providing
CC human gene expression data by subscription, and a computer-readable
CC storage medium which contains a database having a plurality of records
CC (each record including data on the expression of a single exon probe
CC cited above). The probe, methods and apparatus are useful in gene
CC expression analysis. The probes may be used as tools for surveying
CC tissues to detect the presence of expressed messages that contain their
CC specific exon, or in constructing genome-derived single exon microarrays.
CC In addition, the probes are used in identifying and characterising

CC alternative splicing events, in detecting and characterising gross
CC alterations in the genomic locus that includes their exon, in assessing
CC smaller genomic alterations, in priming the synthesis of nucleic acids,
CC or in expressing the ORF-encoded peptide. The present sequence is a human
CC single exon probe of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030194704
XX
SQ Sequence 284 BP; 60 A; 78 C; 74 G; 72 T; 0 U; 0 Other;
Query Match 12.6%; Score 224.8; DB 12; Length 284;
Best Local Similarity 96.0%; Pred. No. 8e-51;
Matches 242; Conservative 0; Mismatches 7; Indels 3; Gaps 1;
QY 500 GTCTGAATCCATACTCTTTGCGATTAAACATCGACACAAAGGATTTCAACGGGCAGAGTA 559
Db 284 GTCCGAATCTCATACTCTTTGCGATTAAACATCGACACAAAGGATTTCAACGGGCAGAGTA 225
QY 560 AGTTTGCTCCACCGTTTCAGACCTCTTAAAGGAGTCAACGCAGAGTCACTCTTGC 619
Db 224 AGTTTGCTCCACCGTTTCAGACCTCTTAAAGGAGTCAACGCAGAGTCACTCTTGC 168
QY 620 TGAAGGAGTCCACGCAAGGAGTGAGCAGCCTGTTCAAGGAGATCACAGCCTCTCTGCCG 679
Db 167 TGAAGGAGTCCACGCAAGGAGTGAGCAGCCTGTTCAAGGAGATCACAGCCTCTCTGCCA 108
QY 680 TCTCCATCTCATCAAACTGAAACAGGAGACCGACCCCTTGCCTGTCGTCCAGGAATG 739
Db 107 TCTCCATCTCATCAAACTGAAACAGGAGACCGACCCCTTGCCTGTCGTCCAGGAATG 48
QY 740 TCAGTGTCTGATG 751
Db 47 TCAGTGTCTGATG 36
RESULT 13
AAS92200
ID AAS92200 standard; cDNA; 463 BP.
XX
AC AAS92200;
XX 13-FEB-2002 (first entry)
XX DNA encoding novel human diagnostic protein #28004.
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX Homo sapiens.
XX WO200175067-A2.
XX 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US008631.
XX 31-MAR-2000; 2000US-00540217.
XX 23-AUG-2000; 2000US-00649167.
XX (HYSE-) HYSEQ INC.
XX Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
XX P-PSDB; ABG28013.
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX Claim 1; SEQ ID NO 28004; 103pp; English.


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OS Homo sapiens.
PN EP1033401-A2.
XX
XX
PD 06-SEP-2000.
XX
XX 21-FEB-2000; 2000EP-00200610.
XX
XX 26-FEB-1999; 99US-0122487P.
XX
XX (GSET ) GENSET.
XX
XX Dumas Milne Edwards J, Duclert A, Giordano J;
XX
XX WPI; 2000-500381/45.
XX
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
XX Claim 1; SEQ ID NO 16002; 71pp + Sequence Listing; English.
XX
XX The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'
CC ESTs are derived from mRNAs with intact 5' ends and can therefore be used
CC to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in
CC diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors
XX
XX SQ Sequence 190 BP; 47 A; 42 C; 73 G; 28 T; 0 U; 0 Other;
Query Match 7.5%; Score 133.4; DB 3; Length 190;
Best Local Similarity 99.3%; Pred. No. 6.2e-26;
Matches 134; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1464 CAGATCACTGCGAAACCTGCTCGACGGTGAGATGGAGCACTACCGCGCTCCGGCAAGA 1523
Db 19 CAGATCACTGCGAAACCTGCTCGACGGTGAGATGGAGCACTACCGCGCTCCGGCAAGA 78
Qy 1524 GGTGGACACCTTGAAGAAGGAGTGGCTGAACAGAGAGCGCGCAGGCGCATGAAGTCCA 1583
Db 79 GGTGGACACCTTGAAGAAGGAGTGGCTGAACAGAGAGCGCGCAGGCGCATGAAGTCCA 138
Qy 1584 GCGCTGCCAGCTA 1598
Db 139 GCGCTGCCAGGTA 153
Search completed: October 26, 2005, 02:00:13
Job time : 987 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 25, 2005, 21:20:38 ; Search time 7722 Seconds
(without alignments)

11181.973 Million cell updates/sec

Title: US-10-070-255-4

Perfect score: 1782

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hlg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	1742	97.8	1906	6	A66645
3	1595	89.5	2873	6	AX089606
4	1595	89.5	3139	6	AX089605
5	1129.8	63.4	2248	6	BD157657
6	1129.8	63.4	2248	6	AX879111
7	1129.8	63.4	2248	9	AX022425
8	937.4	52.6	1033	6	CQ714292
9	818.4	45.9	5833	9	HSM08428
10	816.8	45.8	6045	6	BD160227
11	816.8	45.8	6045	6	AX883269
12	816.8	45.8	6045	9	AX023827
13	694.8	36.7	1229	9	BC041583
14	639.8	35.9	730	6	BD146965
15	639.8	35.9	730	6	AX866903
16	388	21.8	161864	9	AC007601
17	388	21.8	174136	2	AC126766
18	388	21.8	198521	2	AC145723
19	388	21.8	201237	2	AC141081

20	388	21.8	202689	2	AC034281
c 21	373.8	21.0	198703	2	AC144590
22	365.8	20.5	203216	2	AC097328
c 23	364.2	20.4	132333	2	AC138881
24	364.2	20.4	140011	2	AC088864
c 25	364.2	20.4	158388	9	AC008740
26	364.2	20.4	168268	9	AC009124
27	364.2	20.4	171940	9	AC025279
c 28	364.2	20.4	174010	2	AC023814
29	364.2	20.4	178081	2	AC023463
c 30	364.2	20.4	194943	2	AC142201
c 31	364.2	20.4	200812	9	AC133555
32	364.2	20.4	233479	2	AC126758
33	362.6	20.3	156989	2	AC069176
34	305.4	17.1	1431	10	AF399755
c 35	275	15.4	5496	9	AK074072
36	254.4	14.3	198521	2	AC145723
c 37	254.4	14.3	202689	2	AC034281
c 38	254.2	14.3	203216	2	AC097328
39	245.6	13.8	148230	2	AC141548
40	245.6	13.8	165881	2	AC133732
41	245.6	13.8	263443	2	AC121644
42	233	13.1	177955	2	AC131034
c 43	227.8	12.8	156989	2	AC069176
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ALIGNMENTS

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DEFINITION	AX089604					
ACCESSION	AX089604					
VERSION	AX089604.1	GI:13443796				
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AUTHORS						
TITLE						
JOURNAL						
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	/mol_type="unassigned DNA"					
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ORIGIN						
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Best Local Similarity		100.0%	Pred. No. 0;			
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Db	1	ATGACGGGATCACAGACATGCAAAAGACAATTTCTGCTGGAGCGACTGCTGGATGCA	60			
Qy	61	GTGAACACAGTCCAGATCCCGTTTGGAGGAGAAAGAGATTCCTCGGATTCGACAGC	120			
Db	61	GTGAACACAGTCCAGATCCCGTTTGGAGGAGAAAGAGATTCCTCGGATTCGACAGC	120			
Qy	121	AGGTCACCTGTCTGTGTCGCCAGTTTGAAGCCGTCCTGAGATGCTTGAAGAGAGT	180			
Db	121	AGGTCACCTGTCTGTGTCGCCAGTTTGAAGCCGTCCTGAGATGCTTGAAGAGAGT	180			
Qy	181	CGAGGATTGGCACTCAACGCGGCGAGATCAACGCGGCGGCTTTTGCACCAAAACC	240			
Db	181	CGAGGATTGGCACTCAACGCGGCGAGATCAACGCGGCGGCTTTTGCACCAAAACC	240			

```
QY 241 GAAACAGAGCCCGTGTCTGGTACTAGTGAAGGAGGTCTCTCAACAAAGCAAGAGCTGCAG 300
Db 241 GAAACAGAGCCCGTGTCTGGTACTAGTGAAGGAGGTCTCTCAACAAAGCAAGAGCTGCAG 300
QY 301 CGCTTCTACTCCCTCGCCACATCGCTCAGACGTGGCGCGGGTCCGCGCTCGCTCGCG 360
Db 301 CGCTTCTACTCCCTCGCCACATCGCTCAGACGTGGCGCGGGTCCGCGCTCGCTCGCG 360
QY 361 TGTGCCCTCAACGAAACACTCCCTGAGCGCTACTCTGCACATGCTCTCTGCGCGAGCTGC 420
Db 361 TGTGCCCTCAACGAAACACTCCCTGAGCGCTACTCTGCACATGCTCTCTGCGCGAGCTGC 420
QY 421 AGGCTGAGACATTTTATGAAGACTGGTCTTTTGTGATGATGAAGAAAGTCCAGTATG 480
Db 421 AGGCTGAGACATTTTATGAAGACTGGTCTTTTGTGATGATGAAGAAAGTCCAGTATG 480
QY 481 CTTCTACCATGCGCAGAGCTCTGAATCCATCTCTTTGCGATTAAACATCGACAAAG 540
Db 481 CTTCTACCATGCGCAGAGCTCTGAATCCATCTCTTTGCGATTAAACATCGACAAAG 540
QY 541 GATTTGAACGGGCGAGAGTAAAGTTTGTCTCCACCGTTTCAGACCTCTTAAAGGAGTCAACG 600
Db 541 GATTTGAACGGGCGAGAGTAAAGTTTGTCTCCACCGTTTCAGACCTCTTAAAGGAGTCAACG 600
QY 601 CAGAACGTGACCTCTCTGCTGAAGAGTCCACGCAAGAGTGAAGAGCTGTTTCAGGGAG 660
Db 601 CAGAACGTGACCTCTCTGCTGAAGAGTCCACGCAAGAGTGAAGAGCTGTTTCAGGGAG 660
QY 661 ATCAGAGCTCTCTGCGCTCTCCATCTCATCAACCTGAAACAGAGACCGACCCCTTG 720
Db 661 ATCAGAGCTCTCTGCGCTCTCCATCTCATCAACCTGAAACAGAGACCGACCCCTTG 720
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Db 721 CTTGTCTGTCCAGGAATGTCACTGCTGATGCCAAATGCAAAAGAGGCGGAAAGAAA 780
QY 781 AAGAAAGTACCAACATAATCTCATTTGATGATGAGAGAGTGAAGAGTCTCGGGAC 840
Db 781 AAGAAAGTACCAACATAATCTCATTTGATGATGAGAGAGTGAAGAGTCTCGGGAC 840
QY 841 GTGTTTAAAAAGACACTCGGGGAGGAGAGCTCAGAGGACAACTCCGACCGCTCTCT 900
Db 841 GTGTTTAAAAAGACACTCGGGGAGGAGAGCTCAGAGGACAACTCCGACCGCTCTCT 900
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QY 961 AGCAACTCATGGAATTTGATTCCTGCTTTGAAAGGAGTTTGGGTACGAGAGCTT 1020
Db 961 AGCAACTCATGGAATTTGATTCCTGCTTTGAAAGGAGTTTGGGTACGAGAGCTT 1020
QY 1021 GATGTGAAAGAGTATGATGATGAAGTGTGATGAAAGCAAGATGACGTGTATGGAAC 1080
Db 1021 GATGTGAAAGAGTATGATGATGAAGTGTGATGAAAGCAAGATGACGTGTATGGAAC 1080
QY 1081 TCATCAGGAAGGAGACAGAGGCGCACTCGAGTTCGCCGAGAGCCACTGGAAGGGAAC 1140
Db 1081 TCATCAGGAAGGAGACAGAGGCGCACTCGAGTTCGCCGAGAGCCACTGGAAGGGAAC 1140
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RESULT 2

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A66645
LOCUS A66645 1906 bp DNA linear PAT 29-MAR-1999
DEFINITION Sequence 1 from Patent WO9737016.
ACCESSION A66645
VERSION A66645.1 GI:4538138
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 1906)
AUTHORS Wallach,D., Malinin,N., Boldin,M., Kovalenko,A. and Mett,I.
TITLE MODULATORS OF TNF RECEPTOR ASSOCIATED FACTOR (TRAF), THEIR
PREPARATION AND USE
JOURNAL Patent: WO 9737016-A 1 09-OCT-1997;
VEDA RES & DEV (IL)
COMMENT Other publication AU 2175597 19971022.
FEATURES
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RESULT 3
AX089606 LOCUS 2873 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 6 from Patent WO0116314.
ACCESSION AX089606
VERSION AX089606.1 GI:13443798
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Wallach,D., Malinin,N., Sinha,I.W. and Leu,S.
TITLE iren protein, its preparation and use
JOURNAL Patent: WO 0116314-A 6 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT Co. LTD. (IL)
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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AX089605
LOCUS AX089605 3139 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 5 from Patent WO0116314.
ACCESSION AX089605
VERSION AX089605.1 GI:13443797
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Wallach,D., Malinin,N., Sinha,I.W. and Leu,S.
TITLE Iren protein, its preparation and use
JOURNAL Patent: WO 0116314-A 5 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT Co. LTD. (IL)

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Best Local Similarity 100.0%; Pred. No. 0; Indels 0; Gaps 0;
Matches 1595; Conservative 0; Mismatches 0

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LOCUS

AX879111

Sequence 14016 from Patent EP1074617.

AX879111

AX879111.1

GI:40033847

Homo sapiens (human)

Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

Ota, T., Isegai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J., Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T. Primers for synthesising full-length cDNA and their use Patent: EP 1074617-A 14016 07-FEB-2001; (JP) Research Association for Biotechnology (JP) Location/Qualifiers

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Best Local Similarity 95.3%; Pred. No. 3.8e-267;

Matches 1164; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

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DEFINITION AK022425
ACCESSION AK022425
VERSION AK022425.1 Gi:10433818
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1
Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Ohayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahara, K., Murakami, K., Yaeuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoi, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hiraoka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S.,

Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Mueashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Shionata, N., Sano, S., Mori, S., Momiya, H., Satoh, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumaegi, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yanada, K., Fujii, Y., Ozaki, K., Hirao, M., Ohnori, Y., Kawabata, A., Hiki, T., Kobatake, N., Inagaki, H., Ikemura, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigetani, K., Senba, T., Matsunuma, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakamura, Y., Nagahara, K., Masuho, Y., Ninomiya, K., and Iwayanagi, T. NEDO human cDNA sequencing project

Unpublished
3 (bases 1 to 2248)
Isogai, T. and Otsuki, T.
Direct Submission
Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction; 5'- and 3'-end one pass sequencing and clone selection; Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.

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DEFINITION Sequence 236 from Patent WO02068579.
ACCESSION Q714292
VERSION Q714292.1 GI:42275149
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 226 06-SEP-2002;
PE Corporation (NY) (US)
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VERSION BX648280.1 GI:34367439
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AUTHORS Boecker,H., Boecker,M., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
Fobo,G., Han,M. and Wiemann,S.
CONSTRM The German Human cDNA Consortium
TITLE Direct Submission
JOURNAL Submitted (27-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
This clone (DKFZp686E09125) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/proj/cDNA/.
Location/Qualifiers
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DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD160227
VERSION BD160227.1 GI:27865985
SOURCE JP 2002191363-A/15070.
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
TITLE Primer for synthesizing full-length cDNA and use thereof
JOURNAL Patent: JP 2002191363-A 15070 09-JUL-2002;
COMMENT HELIX RESEARCH INSTITUTE
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PD 09-JUL-2002
PF 28-JUL-2000 JP 2000280990
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PI SAITO,
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
PI KEIICHI NAGAI, TETSUJI OTSUKI
PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ 10,
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LOCUS AX883269 6045 bp DNA linear PAT 17-DEC-2003
DEFINITION Sequence 18174 from Patent EP1074617.
ACCESSION AX883269
VERSION AX883269.1 GI:40038170
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
TITLE Primers for synthesizing full-length cDNA and their use
JOURNAL Patent: EP 1074617-A 18174 07-FEB-2001;
RESEARCH Association for Biotechnology
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Best Local Similarity 97.0%; Pred. No. 5.2e-190;
Matches 854; Conservative 0; Mismatches 22; Indels 4; Gaps 2;
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SOURCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
ORGANISM	1 (bases 1 to 1229)
REFERENCE	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altachul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A.C., Rodriguez, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shovenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, A.S., Krzywinski, M.I., Skalska, U., Smalios, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE	22388257
PUBMED	12477932
REFERENCE	2 (bases 1 to 1229)
AUTHORS	Strausberg, R.
TITLE	Direct Submission
JOURNAL	Submitted (20-DEC-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT	Contact: MGC help desk Email: cgabs-r@mail.nih.gov Tissue Procurement: Louis Staudt cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/ Contact: nisc_mgc@hgrl.nih.gov Akhtar, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Hachighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Mastello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsourgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov	
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Best Local Similarity 97.1%; Pred. No. 4.1e-150;
Matches 678; Conservative 0; Mismatches 17; Indels 3; Gaps 1;

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QY 547 AACGGGCAGAGTAAAGTTTGTCTCCACCGTTTTCAGACCTCTTAAAGAGAGTCAACGCAAA 606
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ACCESSION
VERSION
BD146965
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Primer for synthesizing full-length cDNA and use thereof.
BD146965.1 GI:27852723
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KEYWORDS JP 2002191363-A/1808.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,
JOURNAL Iehii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002191363-A 1808 09-JUL-2002;
HELIX RESEARCH INSTITUTE
COMMENT OS Homo sapiens (human)
PN JP 2002191363-A/1808
PD 09-JUL-2002
PF 28-JUL-2000 JP 2000280990
PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
PI SAIJO, JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
PI KEIICHI NAGAI, TETSUJI OTSUKI
PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10,
C12N5/09, C12P21/02, C12P21/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
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Best Local Similarity 99.0%; Pred. No. 2e-146;
Matches 663; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

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LOCUS AX866903 730 bp DNA linear PAT 17-DEC-2003
DEFINITION Sequence 1808 from Patent EP1074617.
ACCESSION AX866903
VERSION AX866903.1 GI:40021252
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayaishi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
TITLE Primers for synthesizing full-length cDNA and their use
JOURNAL Patent: EP 1074617-A 1808 07-FEB-2001;
Research Association for Biotechnology (JP)
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Best Local Similarity 99.0%; Pred. No. 2e-146;
Matches 663; Conservative 0; Mismatches 5; Indels 2; Gaps 2;
QY 1 ATGAGCGGATCACAGAACATGACAAAGACAATTTCTGCTGGAGCGACTGCTGGATGCA 60
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